

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:46:53 ; Search time 176 Seconds  
(Without alignments)  
5169.360 Million cell updates/sec

Title: US-09-975-842-1

Perfect score: 404  
Sequence: 1 ggggtcgcgggggttcaggat.....cccgcctacttaagctctg 404

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_101002:\*  
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
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3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
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9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
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22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 194.8 | 48.2        | 1743   | 19    | AAV30330    |
| 2          | 107.6 | 26.6        | 748    | 24    | AB065439    |
| 3          | 98    | 24.3        | 1384   | 17    | AAAT33136   |
| 4          | 93.2  | 23.1        | 3438   | 20    | AAK35671    |
| 5          | 86.6  | 21.6        | 961    | 19    | AAV000220   |
| 6          | 84.6  | 20.9        | 968    | 19    | AAV000219   |
| 7          | 83.6  | 20.7        | 1170   | 18    | AAAT66247   |
| 8          | 83.6  | 20.7        | 1878   | 19    | AAV30326    |
| 9          | 82.2  | 20.3        | 993    | 17    | AAAT33139   |

|    |      |      |       |    |           |                      |
|----|------|------|-------|----|-----------|----------------------|
| 10 | 82   | 20.3 | 1868  | 18 | AAAT73502 | Poplar 1-aminocycl   |
| 11 | 80.8 | 20.0 | 1864  | 18 | AAAT73501 | Poplar 1-aminocycl   |
| 12 | 80.4 | 19.9 | 1096  | 18 | AAAT72631 | Mangifera indica A   |
| 13 | 80.4 | 19.9 | 1113  | 18 | AAAT72632 | Mangifera indica A   |
| 14 | 78.8 | 19.5 | 1712  | 20 | AAK27501  | Banana 1-aminocycl   |
| 15 | 78.8 | 19.5 | 1712  | 22 | AAK27501  | Banana 1-aminocycl   |
| 16 | 77.7 | 19.1 | 1080  | 18 | AAAT72628 | DNA encoding 1-ami   |
| 17 | 72.4 | 17.9 | 1087  | 17 | AAAT72628 | Arabidopsis thaliana |
| 18 | 72.4 | 17.9 | 1942  | 17 | AAAT38857 | Arabidopsis thaliana |
| 19 | 72.4 | 17.9 | 1945  | 17 | AAAT38856 | Arabidopsis thaliana |
| 20 | 72.4 | 17.9 | 2088  | 19 | AAV20947  | Pelargonium 1-amin   |
| 21 | 72.4 | 17.9 | 2678  | 19 | AAV20947  | Pelargonium 1-amin   |
| 22 | 69.2 | 17.1 | 1482  | 13 | AAQ25896  | Coffea-frut spec     |
| 23 | 69.2 | 17.1 | 1934  | 18 | AAAT6246  | ACC synthase gen     |
| 24 | 67.6 | 16.7 | 1703  | 12 | AAQ15131  | ACC synthase GAC-1   |
| 25 | 67.6 | 16.7 | 1703  | 19 | AAV15701  | Clone PAC1 encodi    |
| 26 | 67.6 | 16.7 | 1703  | 22 | AAV15701  | Zucchini 1-aminoc    |
| 27 | 67.6 | 16.7 | 1703  | 22 | AAV15701  | Zucchini 1-aminoc    |
| 28 | 67.6 | 16.7 | 1923  | 21 | AAZ94267  | Zucchini 1-aminoc    |
| 29 | 65   | 16.1 | 7241  | 12 | AAQ15140  | Mung bean ACC synt   |
| 30 | 64.4 | 15.9 | 1104  | 18 | AAAT72629 | Genomic clone LE-A   |
| 31 | 64.4 | 15.9 | 1775  | 12 | AAQ15134  | Carica papaya ACC    |
| 32 | 64.4 | 15.9 | 1818  | 22 | AAQ15134  | Carica papaya ACC    |
| 33 | 64.4 | 15.9 | 2230  | 19 | AAV15704  | Tomato 1-aminocycl   |
| 34 | 64.4 | 15.9 | 2230  | 22 | AAQ15134  | Tomato 1-aminocycl   |
| 35 | 64.4 | 15.9 | 2230  | 22 | AAQ15134  | Tomato 1-aminocycl   |
| 36 | 64.4 | 15.9 | 7244  | 19 | AAV15705  | Tomato 1-aminocycl   |
| 37 | 64.4 | 15.9 | 7244  | 22 | AAQ15134  | Tomato 1-aminocycl   |
| 38 | 64.4 | 15.9 | 7244  | 22 | AAQ15134  | Tomato 1-aminocycl   |
| 39 | 63.2 | 15.6 | 5613  | 15 | AAQ63241  | Tomato ACC synthas   |
| 40 | 62.8 | 15.5 | 15397 | 18 | AAAT58635 | Cruifer 1-aminoc     |
| 41 | 62.8 | 15.5 | 15397 | 18 | AAAT58635 | T-DNA insert of 13   |
| 42 | 61.2 | 15.1 | 1800  | 19 | AAV09713  | ACC synthase DNA     |
| 43 | 59.6 | 14.8 | 1888  | 19 | AAV31482  | Papaya ACC synthas   |
| 44 | 58.4 | 14.5 | 1098  | 18 | AAAT2630  | Carica papaya ACC    |
| 45 | 48.2 | 11.9 | 7587  | 12 | AAQ15133  | Zucchini ACC synth   |

#### ALIGNMENTS

|          |  |  |
|----------|--|--|
| RESULT 1 | AAV30330   | standard; cDNA; 1743 bp.                       |
| ID       | AAV30330   |  |
| XX       | AAV30330;  |  |
| AC       | 28-SEP-1998  | (first entry)                                  |
| XX       |  |  |
| DT       |  |  |
| XX       |  |  |
| DE       |  |  |
| XX       |  |  |
| KW       | ACC synthase: 1-aminocyclopropane-1-carboxylate synthase;  |  |
| KW       | ethylene; transgenic plant; wilting; rose; prosekacc7; ss. |  |
| XX       |  |  |
| OS       | Rosa sp. cv. Cardinal Red.                                 |  |
| XX       |  |  |
| FH       | Location/Qualifiers  |  |
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| FT       | misc_feature   | complement (1..50)                             |
| FT       |  | /*tag= c                                       |
| FT       | misc_feature   | /*note= "antisense oligonucleotide (Claim 18)" |
| FT       |  | /*tag= d                                       |
| FT       | misc_feature   | complement (51..100)                           |
| FT       |  | /*tag= e                                       |
| FT       | misc_feature   | /*note= "antisense oligonucleotide (Claim 18)" |
| FT       |  | /*tag= f                                       |
| FT       | misc_feature   | complement (101..150)                          |
| FT       |  | /*tag= g                                       |
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| FT       |  | /*tag= h                                       |
| FT       | misc_feature   | complement (151..200)                          |
| FT       |  | /*tag= i                                       |
| FT       | misc_feature   | /*note= "antisense oligonucleotide (Claim 18)" |
| FT       |  | complement (201..250)                          |
| FT       |  | /*tag= g                                       |

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FT      /note= "antisense oligonucleotide (claim 18)"
FT      complement (251..300)
FT      /tag= h
FT      /note= "antisense oligonucleotide (claim 18)"
FT      complement (301..350)
FT      /tag= i
FT      /note= "antisense oligonucleotide (claim 18)"
FT      complement (351..400)
FT      /tag= j
FT      /note= "antisense oligonucleotide (claim 18)"
FT      complement (401..450)
FT      /tag= k
FT      /note= "antisense oligonucleotide (claim 18)"
FT      complement (451..500)
FT      /tag= l
FT      /note= "antisense oligonucleotide (claim 18)"
FT      complement (1..1945)
FT      /tag= m
FT      /note= "any contiguous 50 nucleotides (claim 18)"

XX      WO9814465-A1.
XX      09-APR-1998.
XX      30-SEP-1997; 97WO-US17644.
XX      01-OCT-1996; 96US-0724194.
XX      (COLS ) UNITV COLORADO STATE RES. FOUND.
XX      Ranu RS;
XX      WPI; 1998-260994/23.
XX      P-PSDB; AAM60239.
XX      New isolated ACC synthase genes - are obtained from geranium and
XX      rose, used to develop products for producing plants with reduced
XX      ethylene levels, for increasing shelf-life
XX      Claim 6; Fig 9; 77pp: English.
XX      This cDNA clone, designated Prosekacc7, codes for a
XX      1-aminocyclopropane-1-carboxylate synthase (ACC synthase) (see
XX      AAM60239) of rose (cv. Red Cardinal). High quality mRNA was obtained
XX      from flower tissue using a novel adaptation of the 2-butoxyethanol
XX      precipitation technique. This was converted to cDNA and screened
XX      with a probe generated by PCR amplification (see AAV30328-29). The
XX      Prosekacc7 clone was obtained. 3 geranium ACC synthase clones (see
XX      AAV30324-26) are also claimed. The ACC synthase genes, or their
XX      fragments, when introduced in antisense orientation under control
XX      of a strong promoter, can be used to genetically modify a plant,
XX      especially geranium, rose or woody plant. As a consequence, the
XX      amount of ACC synthase produced in the plant cells is reduced and
XX      the rate of ACC conversion to ethylene decreases. This can be used
XX      to prolong the shelf-life of cut flowers and to reduce leaf
XX      yellowing and petal abscission during shipping and storage.
XX      Sequence 1743 BP; 429 A; 401 C; 442 G; 471 T; 0 other:
XX      Query Match      48.2%; Score 194.8; DB 19; Length 1743;
XX      Best Local Similarity 71.2%; Pred. No. 9.8e-58;
XX      Matches 285; Conservative 0; Mismatches 112; Indels 3; Gaps 2;
```

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Db      1352 TTTCAGACACCAAAATTATGCAATGATCGAGATTAAACAGAAAAGCCTCCGTGAA 1411
Oy      185 TGTACGCTGCATTTGCTGGCGGGGTTGAGAAACTCGGCATCCGATGACGGAAGAGC 244
Db      1412 TGTATCTTAGATTGTGTGAC -AGGATTGAAGCAATTGGCATTTGAGTGCACAAAGCAAT 1470
Oy      245 GGAGGCTTCCTATTGTTGGGCCGACATGACGGGATTCGATTCCTACAGCAAAAAG 304
Db      1471 GGGGG--TTTCTACTGTTGGGCAAGCTTGAGTGGGTTATTCGCTTACAGTAGAAG 1528
Oy      305 GAGAGCTCGACCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAAGTTACTCCGTT 364
Db      1529 GGGAGCTTGACCTCGGAGATAGTTGTGAATGTAGGTAAAGCTCAATGTACTCTGGAT 1588
Oy      365 CTGTGTCATTTGATTTGAACCCGGCTTACTTACGCTGTG 404
Db      1589 CTCTGTGCAATGTGATGTGAACCGGAGATGCTCCGTTTGG 1628

RESULT 2
AB065438/C
ID      AB065439 standard; DNA; 748 BP.
XX      AB065439;
XX      21-AUG-2002 (first entry)
XX      Arabidopsis thaliana polynucleotide SEQ ID NO 16.
XX      Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
XX      stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
XX      insecticide; antibiotic; ds.
XX      Arabidopsis thaliana.
XX      US2002059663-A1.
XX      16-MAY-2002.
XX      26-JAN-2001; 2001US-0770149.
XX      27-JAN-2000; 2000US-178506P.
XX      (GORL/) GORLACH J.
XX      (ANY/) AN Y.
XX      (HAM/) HAMILTON C M.
XX      (PRIC/) PRICE J L.
XX      (RAIN/) RAINES T M.
XX      (YUY/) YU Y.
XX      (RAME/) RAMEKA J G.
XX      (PAGE/) PAGE A.
XX      (MATH/) MATHEW A V.
XX      (LEDF/) LEDFORD B L.
XX      (WESS/) WOEISSNER J F.
XX      (HAAS/) HAAS W D.
XX      (GARC/) GARCIA C A.
XX      (KRIC/) KRICKER M.
XX      (SLAT/) SLATER T.
XX      (DAVI/) DAVIS K R.
XX      (ALIE/) ALLEN K.
XX      (HOFF/) HOFFMAN N.
XX      (HURB/) HURBAN P.
XX      Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
XX      Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
XX      Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N,
XX      Hurlban P;
XX      WPI; 2002-479224/51.
XX      New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
XX      useful e.g. for preparing transgenic plants with increased resistance
XX      or altered metabolism -
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XX Claim 1; SEQ ID NO 16; 40bp + Sequence Listing; English.
PS
CC The invention relates to nucleic acids (I) that hybridise under stringent
CC conditions to any of 999 sequences (AB085424-AB086422) or their
CC fragments, (1) are used to express the corresponding polypeptides (11) or
CC to produce genetically modified plant cells or transgenic plants, which
CC may have improved resistance to disease or stress, or altered
CC metabolic/biosynthetic pathways (for production of commercial,
CC nutritional or medicinal products), or generally any trait of interest,
CC or can be used to screen for biologically active agents (e.g. fungicides,
CC insecticides and antibiotics).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO at seqdata.uspto.gov/sequence.html?docid=99990970149.
XX
SQ Sequence 748 BP; 209 A; 202 C; 120 G; 213 T; 4 other;
Query Match 26.6%; Score 107.6; DB 24; Length 748;
Best Local Similarity 57.4%; Pred. No. 3.2e-27;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;
QY 1 GGGTTGCCGG-3GTTACAGATGGCGGTTATCTACTCTACACAGAAAGCTGCTCACTACT 60
   || || || || || || || || || || || || || || || || || || || || ||
Db 617 GGTCTTCCTCGTTCCCGCTGGGAACATATATCTGTAACAAGATATGTTGTCGGACA 558
QY 61 GCCAAAAGTTGACGAGATTTTCATCTCATCTTCAGCTCCGACGCGCTTCTCTGCTT 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 557 GCGGAAAGAGATGTCGAGCTTCACGCTTGTCTGCTCTACAGACAACTATGCTGGCTTCT 498
QY 121 ATGCTTCGGACACGCGGTTCACTCAAAAGTTTCATCGAGTTAAACAGAGCAAACTGAAA 180
   || || || || || || || || || || || || || || || || || || || || ||
Db 497 ATGTTTCGCGATGATGAGATTACGAGAAAGTACATAGATTAACCGGAAAGACTTGA 438
QY 181 AGAATGTACG-TGCATTCGCGCGGGTTGAAGAAATCGCGATCCGATCAGCGAAAG 240
   || || || || || || || || || || || || || || || || || || || || ||
Db 437 AGACGATACGATTCACATTTGAGAAAGGCTT-AAAGAGCGAAGGATTAAGTGTGGAAGG 379
QY 241 CAGCGGAGGCTTCTCTATTTGTTGGGCGACATGAGCGGATTCGATCCTACAGCGAA 300
   || || || || || || || || || || || || || || || || || || || || ||
Db 378 GAACGCGAGG--GCTATATTTTGTGGATGAATTTGGGTTTCTGCGAAAGAAACTAAAA 321
QY 301 AAAGAGAGACTCGAGCTATGAGCAATGTTGCTAAACATTTGCTAAGTAAACGTTACTCCC 360
   || || || || || || || || || || || || || || || || || || || || ||
Db 320 GAGCGGAGCTCCAGCTTTGGGATGTATCTTAAGAGCTGAACCTGAATATATCTCCG 261
QY 361 GGTTCCTGTTTCTCATTTGTTAATGAACCGGCTACTTTAGCCTCTG 404
   || || || || || || || || || || || || || || || || || || || || ||
Db 260 GGAATCTTCGTTCCACTGCTCGAGGTGAGTGTGTTAGGGCTTG 217
.
RESULT 3
AAAT33136
ID AAAT33136 standard; DNA; 1384 BP.
XX
AC AAAT33136;
XX
DT 07-DEC-1996 (First entry)
XX
DE Broccoli ACC synthase genomic DNA clone ACCA1.
XX
KM ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase;
KM ethylene; shell-life; Cucumis melo; melon; transgenic plant;
KM antisense; broccoli; ss.
OS Brassica oleracea.
XX
FH Key Location/Qualifiers
FT primer_bind complement (1..31)
FT /tag= a
FT /note= "primer RMM393"
FT 1..37
FT exon
FT /tag= b

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FT intron
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FT 38..134
FT /*tag= c
FT exon
FT 135..431
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FT 432..594
FT /*tag= e
FT exon
FT 595..1384
FT /*tag= f
FT primer_bind 1352..1382
FT /*tag= g
FT /note= "primer RMM394"
.
WO9621027-A1.
XX
PD 11-JUL-1996.
XX
PE 07-JUN-1995; 95WO-US07271.
XX
PR 30-DEC-1994; 94US-0366992.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, Carney KJ, Deng RZ, Reynolds JF, Ruttenclutter GE;
XX P-PSDB; AAR98598.
XX
DR WPI: 1996-334002/33.
XX
PT DNA encoding 1-aminocyclopropyl-1-carboxylic acid synthase of
PT Brassica oleracea - used to regulate ethylene-dependent processes
PT in plants, esp. to improve shelf life
XX
PS Claim 2; Fig1A-B; 50pp; English.
.
CC Brassica oleracea genomic clone ACCA1 (AAAT33136) codes for
CC 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase)
CC (AAR98598), an enzyme involved in ethylene biosynthesis. It was
CC obt. by subjecting broccoli leaf total genomic DNA to PCR using
CC primers (see also AAAT33137-38) based on the Arabidopsis thaliana ACC
CC synthase gene. The product was cloned into pCRII to obtain clone
CC ACCA1. Genomic DNA or cDNA (see also AAAT33139) can be inserted, in
CC sense or antisense orientation, into an expression cassette and then
CC transferred to a binary vector suitable for Agrobacterium-mediated
CC plant transformation. The constructs permit control of the level of
CC ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
CC melo) and hence a control of maturation, ageing and shelf-life.
XX
SQ Sequence 1384 BP; 401 A; 290 C; 310 G; 383 T; 0 other;
Query Match 24.3%; Score 98; DB 17; Length 1384;
Best Local Similarity 55.9%; Pred. No. 1.1e-23;
Matches 226; Conservative 0; Mismatches 175; Indels 3; Gaps 2;
QY 1 GGGTTGCCGGGTTACAGATGGCGGTTATCTACTCTACACAGAGAGTCTCACTACT 60
   || || || || || || || || || || || || || || || || || || || || ||
Db 970 GGTCTTCCTCGTTCCCGCTGGGAACATATATCTGTAACAAGATATGTTGTCGACA 1029
QY 61 GCCAAAAGTTGACGAGATTTTCATCTCATCTTCAGCTCCGACGCGCGCTTCTCTGCTT 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 1030 GCGAAGAGGATGCGAATTTTCACGCTTGTCTGCTGACACAAACATGTTGCTTCC 1089
QY 121 ATGCTTCGGACACGCGGTTCACTCAAAAGTTTCATCGAGTTAAACAGCAACTCAAA 180
   || || || || || || || || || || || || || || || || || || || || ||
Db 1090 ATGTTTCGCGATGGAAGATTTCAGGAGATTAAGATTAACCGTGAAGGCTTAGG 1149
QY 181 AGAATGTACGCTGATTCGCGGCGCGGTTGAAGAAACTGCGCTTCGATGACAGGAAG 240
   || || || || || || || || || || || || || || || || || || || || ||
Db 1150 AGACGATACGACAAATTTGGGAAGGCTT-AAAGAACGAGGAGTTCAAGTGTGGAAGG 1208
QY 241 CAGCGGAGGCTTCTCATTTGTTGGGCGACATGAGCGGATTCGATCCTACAGCGAA 300
   || || || || || || || || || || || || || || || || || || || || ||
Db 1209 TAATGACAGGT--TGTTCTGTGGATGAATTTGGGTTTCTTGCTCGACAGCAAAACGAAA 1266

```

[illegible]

|          |  |   |      |
|----------|--|---|------|
| Db       | 2414   | TTATTATCTGTGACAAGAGTTCTACTAAGAACTACCTTAGAGAGAACCAAAAACGGGCTCAG  | 2473 |
| Oy       | 181  | AGAAATGTACGGCTGCATTCGTGTGGGGGGGTTGAAGAAACTGGCATCCGATCGACGGAAAG  | 240  |
| Db       | 2474   | AACGACAGAGAAAGAGCTCGTGGTTGGGTTCTAGAGGCCA-TGGGATCAAAATGTTGMAAG   | 2532 |
| Oy       | 241  | CAGCGGAGGCTTCCTCTATTGTGTGGGGCCGACATGAGCGGATTTGATTCGATCCACAGCGAA | 300  |
| Db       | 2533   | TAAATCCGGG--ACCTCTTTTGTGGGTGACATGACCTCTCTAGATCTTAAACGTTTC       | 2590 |
| Oy       | 301  | AAAGAGAGCTCGAGCATGTGGAGCAAGTTGCTTAAACATTTAGAGTAAAGCTTACTCC      | 360  |
| Db       | 2551   | GAAAGGAAATGATCTTTGTGGAAAGAGATTGTTTACGAGTGAAGTCAACATCTCTCT       | 2650 |
| Oy       | 361  | GGTCTTGTGTCTCAATGTATTTGAACCCGGGCTACTTAAAGCCTCTG                 | 404  |
| Db       | 2651   | GGTTCGTGCTGCATTTGTGAAGAACCGGTTGGTTAGAGTTTG                      | 2694 |
| RESULT 5 |  |   |      |
| AAV00220 |  |   |      |
| ID       | AAV00220   | standard; DNA; 961 BP.  |      |
| XX       |  |   |      |
| AC       | AAV00220;  |   |      |
| XX       |  |   |      |
| DT       | 08-JUN-1998  | (first entry)   |      |
| XX       |  |   |      |
| DE       | 1-aminocyclopropane-1-carboxylic acid synthase gene acacc3.        |   |      |
| XX       |  |   |      |
| KM       | 1-aminocyclopropane-1-carboxylic acid: ACC synthase; pineapple;    |   |      |
| KM       | flowering; inhibition; regulation; development; fruit; ss.         |   |      |
| XX       |  |   |      |
| OS       | Ananas comosus.  |   |      |
| XX       |  |   |      |
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| FT       |  | /product= "acacc3"  |      |
| FT       |  | /note= "no stop codon given; contains an intron"                |      |
| FT       | exon   | 1..101  |      |
| FT       |  | /*tag= b  |      |
| FT       |  | /number= 1  |      |
| FT       | intron   | 102..193  |      |
| FT       |  | /*tag= c  |      |
| FT       |  | /number= 1  |      |
| FT       | exon   | 194..961  |      |
| FT       |  | /*tag= d  |      |
| FT       |  | /number= 2  |      |
| XX       |  |   |      |
| PN       | AU9719963-A.   |   |      |
| XX       |  |   |      |
| PD       | 06-NOV-1997.   |   |      |
| XX       |  |   |      |
| PF       | 01-MAY-1997;   | 97AU-001963.  |      |
| XX       |  |   |      |
| PR       | 01-MAY-1996;   | 96AU-0009582.   |      |
| XX       |  |   |      |
| PA       | (GOLD-) GOLDEN CIRCLE LTD.   |   |      |
| PA       | (QUEE-) STATE QUEENSLAND.  |   |      |
| PA       | (UYOU ) UNIV QUEENSLAND.   |   |      |
| XX       |  |   |      |
| PI       | Botella J, Sanewski G;   |   |      |
| XX       |  |   |      |
| DR       | WPI; 1998-009279/02.   |   |      |
| XX       |  |   |      |
| DR       | P-PSDB; AAW37445.  |   |      |
| PT       | New isolated ACC synthase genes from pineapples - used to generate |   |      |
| PT       | transgenic pineapples in which the natural initiation of flowering |   |      |
| PT       | is inhibited   |   |      |
| XX       |  |   |      |
| PS       | Claim 2; Fig 2; 37pp; English.                                     |   |      |
| XX       |  |   |      |
| CC       | The present sequence represents the nucleotide sequence encoding a |   |      |



|                           |  |
|---------------------------|--|
| DE                        | ACC synthase GAC-2 DNA.  |
| XX                        |  |
| KW                        | ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; antisense;     |
| KM                        | ethylene; transgenic plant; Pelargonium x domesticum;                    |
| KW                        | in vitro propagation; tissue culture; ripening; ss.                      |
| XX                        |  |
| OS                        | Not identified.  |
| XX                        |  |
| PN                        | M09717429-A1.  |
| XX                        |  |
| PD                        | 15-MAY-1997.   |
| XX                        |  |
| PE                        | 08-NOV-1996; 96WO-US17954.   |
| XX                        |  |
| PR                        | 09-NOV-1995; 95US-0555755.   |
| XX                        |  |
| PA                        | (OGLE-) OGLEVEE LTD.   |
| PA                        | (PENN-) PENN STATE RES FOUND.  |
| XX                        |  |
| PI                        | Arteca J, Arteca RN, Ogilevee-O'Donovan W, Skoots E;                     |
| DR                        | WI: 1997-281019/25.  |
| DR                        | P-PsDB; AAM09879.  |
| XX                        |  |
| PT                        | Commercial propagation of transgenic plants by tissue culture -          |
| PT                        | especially Pelargonium x domesticum with decreased ethylene              |
| PT                        | formation  |
| XX                        |  |
| PS                        | Claim 14; Page 24; 36pp: English.  |
| XX                        |  |
| CC                        | 2 DNA sequences (AAT66246-47) respectively code for                      |
| CC                        | 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1           |
| CC                        | (AAM09878) and GAC-2 (AAM09879), enzymes involved in the biosynthesis    |
| CC                        | of ethylene in plants. In a method for the commercial production         |
| CC                        | of transgenic plants, Agrobacterium vectors carrying antisense           |
| CC                        | genes for ACC synthase or ACC oxidase (see also AAT66248) are used       |
| CC                        | to inoculate petiole explants of a mother plant, pref-                   |
| CC                        | erably Pelargonium x domesticum. The resulting callus is cultured and    |
| CC                        | used to regenerate transgenic plants. The antisense genes prevent        |
| CC                        | ACC synthase or ACC oxidase expression and hence ethylene                |
| CC                        | formation and fruit ripening.  |
| XX                        |  |
| SQ                        | Sequence 1170 BP; 319 A; 263 C; 297 G; 291 T; 0 other:                   |
| Query Match               | 20.7%; Score 83.6; DB 18; Length 1170;                                   |
| Best Local Similarity     | 53.7%; Pred. No. 1.2e-18;  |
| Matches 217; Conservative | 0; Mismatches 184; Indels 3; Gaps  |
| OY                        | 1 GGCTGGCCGGGTTAGCATGGCGCTTATCTACTCTCAACAGAGAAGTCGTCTACTACT 60           |
| DB                        | 2.   |
| OY                        | 763 GGCTTCCTCGCTTAGGGTGGGGAATTGTCTACTCTCAACATGACGCAGATTGTGATTTGT 822     |
| OY                        | 61 GCCAAAGATGACAGATTTTTCATTCATTCAGCTCCGAGCAGAGCGCTTGCTGCTGTT 120         |
| DB                        |  |
| OY                        | 823 GCGCAAAGATGTCAAGTTTCGCCCTGTGATCCACAACAACTCAGCACCTAATCGCATCA 882      |
| OY                        | 121 ATGCTCTGGGACACCGCGGTCTCACTAAAAGTCAATCGAGGTAAACAGACGSAACTCMAA 180     |
| DB                        |  |
| OY                        | 883 ATGCTCTGGACAGATGAATAATTCGTGGACACATTCATCTGTGGAGAGGCGCAGAGGCTACGC 942  |
| OY                        | 181 AGAATGTACCGCTGCATTCGTGTGGCGGGGTTGAAGAACTCGGCATTCGATGACGGAAG 240      |
| DB                        |  |
| OY                        | 943 AGAAGTACCGCAACTTCCACAGAGGGCGTTGCA-CAGTCCACATTTGGGAGCGCTTAAGAG 1001   |
| OY                        | 241 CAGCGAGGCTTCTCTATTGTTGGGCCGACATGAGCGCATTTATTTCGATCTACAGCGAA 300      |
| DB                        |  |
| OY                        | 1002 CAATGGGGGGATTATTCAT--ATGGATGGACTTGAGAGAGGCTTCTCAAGGAGAAGACTTTC 1059 |
| OY                        | 301 AAAGAGAGCTGAGCTATNGGACAAGTGTCAAAACATTTGTAAGGTAAACGTTACTCTCC 360      |
| DB                        |  |
| OY                        | 1060 GAGGCGGAGATGCTCTGTGGAGAGTGAATATCAATGAGGTAAAGTAAATGTGTGCCA 1119      |
| OY                        | 361 GGTTCCTTGTCATTGTAATTGACCGCGCTACTTAAAGCCTCTG 404                      |

| Db       | 1120   | GGGCGCTTCATTCGCGAGCAGGTCGTCAAGTCTG                | 1163 |
|----------|--|---|------|
| RESULT 8 |  |   |      |
| ID       | AAV30326   | standard; cDNA: 1878 BP.                          |      |
| AC       | AAV30326;  |   |      |
| XX       |  |   |      |
| DT       | 28-SEP-1998  | (first entry)                                     |      |
| XX       |  |   |      |
| DE       | Pelargonium 1-aminocyclopropane-1-carboxylase synthase cDNA. |   |      |
| XX       |  |   |      |
| KW       | ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;    |   |      |
| RW       | ethylene; transgenic plant; wilting; geranium; pHSacc49; ss. |   |      |
| XX       |  |   |      |
| OS       | Pelargonium x hortorum cv. Sincerity.                        |   |      |
| XX       |  |   |      |
| FH       | Key  | Location/Qualifiers                               |      |
| FI       | CDS  | 104..1576   |      |
| FI       |  | /*tag= a  |      |
| FI       | polyA_signal   | 1810..1815  |      |
| FI       |  | /*tag= b  |      |
| FI       | misc_feature   | complement (1..50)                                |      |
| FI       |  | /*tag= c  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (51..100)                              |      |
| FI       |  | /*tag= d  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (101..150)                             |      |
| FI       |  | /*tag= e  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (151..200)                             |      |
| FI       |  | /*tag= f  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (201..250)                             |      |
| FI       |  | /*tag= g  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (251..300)                             |      |
| FI       |  | /*tag= h  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (301..350)                             |      |
| FI       |  | /*tag= i  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (351..400)                             |      |
| FI       |  | /*tag= j  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (401..450)                             |      |
| FI       |  | /*tag= k  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (451..500)                             |      |
| FI       |  | /*tag= l  |      |
| FI       |  | /note= "antisense oligonucleotide (claim 13)"     |      |
| FI       | misc_feature   | complement (1..1878)                              |      |
| FI       |  | /*tag= m  |      |
| FI       |  | /note= "any contiguous 50 nucleotides (claim 13)" |      |
| XX       |  |   |      |
| PN       | W09814465-A1.  |   |      |
| XX       |  |   |      |
| PD       | 09-APR-1998.   |   |      |
| XX       |  |   |      |
| PF       | 30-SEP-1997;   | 97WO-US17644.                                     |      |
| XX       |  |   |      |
| PR       | 01-OCT-1996;   | 96US-0724194.                                     |      |
| XX       |  |   |      |
| PA       | (COLS ) UNIV COLORADO STATE RES FOUND.                       |   |      |
| XX       |  |   |      |
| PI       | Ranu RS;   |   |      |
| XX       |  |   |      |
| DR       | WPI: 1998-260994/23.   |   |      |
| XX       |  |   |      |
| DR       | P-PSDB; AAM60235.  |   |      |

PT New isolated ACC synthase genes - are obtained from geranium and  
PT rose, used to develop products for producing plants with reduced  
PT ethylene levels, for increasing shelf-life

PS Claim 1; Fig 5; 77pp; English.

CC This cDNA clone, designated pPHSacc49 (ATCC 98179), codes for a  
CC 55.1 kDa 1-aminocyclopropane-1-carboxylate synthase (ACC synthase)  
CC (see AA060235) of geranium (*Pelargonium x hortorum* cv. *Sincerely*).  
CC High quality mRNA was obtained from flower tissue using a novel  
CC adaptation of the 2-butoxyethanol precipitation technique. This  
CC was converted to cDNA and screened with a probe generated by PCR  
CC amplification (see AA03028-29). The pPHSacc49 clone was obtained.  
CC Geranium ACC synthase cDNA clones pHSacc41 (see AA03024) and  
CC pHSacc44 (see AA03025), and rose ACC synthase cDNA clone prosekao  
CC (see AA030330), are also claimed. These ACC synthase genes, or their  
CC fragments, when introduced in antisense orientation under control  
CC of a strong promoter, can be used to genetically modify a plant,  
CC especially geranium, rose or woody plant. As a consequence, the  
CC amount of ACC synthase produced in the plant cells is reduced and  
CC the rate of ACC conversion to ethylene decreases. This can be used  
CC to prolong the shelf-life of cut flowers and to reduce leaf  
CC yellowing and petal abscission during shipping and storage.

Sequence 1878 BP; 569 A; 390 C; 432 G; 487 T; 0 other;

|             |  |
|-------------|--|
| Query Match | 20.78; Score 83.6; DB 19; Length 1878; |
|-------------|--|

Best Local Similarity 53.7%; Pred. No. 1.5e-18;  
Matches 217; Conservative 0; Mismatches 184

Matches 217; Conservative 0; Mismatches 184; Indels 3; Gaps 2.

|    |      |        |           |            |          |          |          |           |         |         |        |        |        |       |     |      |      |
|----|------|--------|-----------|------------|----------|----------|----------|-----------|---------|---------|--------|--------|--------|-------|-----|------|------|
| OY | 1    | GGGTGC | CGGSGTTCA | GAGATGGC   | GTTATTC  | TACTCTAC | A        | CAGAGA    | AGTGCT  | CACTACT | 60     |        |        |       |     |      |      |
| Db | 953  | GGCTTC | CCCTGGCTT | CAGGGGGGA  | TGTCTACT | CTCAAA   | TAGACAG  | AGTTGT    | GAATTGT | 1012Z   |        |        |        |       |     |      |      |
| OY | 61   | GCCAAA | AGTTGAG   | AGATTTT    | CATTCAT  | TACGTG   | CGAGCAG  | CGGCTG    | CTGCTG  | 120     |        |        |        |       |     |      |      |
| Db | 1013 | GCGGAA | AGATG     | TCAAAGTTT  | CGGCC    | TTGTA    | TCCACA   | CAAAC     | TACAC   | 1072Z   |        |        |        |       |     |      |      |
| OY | 121  | ATGCTT | CGGACAG   | CGCGGTT    | CAC      | TCTCA    | CAAAAGTT | CATG      | SAGSTA  | MAACGAG | CGAAGT | CAAA   | 180    |       |     |      |      |
| Db | 1073 | ATGCTC | CGGACAG   | TGAAT      | TCG      | GSAC     | ACATTC   | ATCAT     | GTG     | SAGS    | AGCGCA | AGAGG  | CTAACG | 1132Z |     |      |      |
| OY | 181  | AGAAT  | TACCTGC   | ATTCTG     | TGGCG    | GGGGTT   | GAA      | GAATACT   | CGGCAT  | CCGATG  | CA     | CGGAAG | 240    |       |     |      |      |
| Db | 1133 | AGAA   | GTTCAC    | CAACC      | CTTCTCAC | AAAGGG   | CTT      | TGCA - CA | AGTAAC  | ATTGAT  | GCTCA  | AAAG   | 1191D  |       |     |      |      |
| OY | 241  | CAGG   | AGGCTCT   | CTATTG     | TGTTGG   | CGCAG    | CA       | TAGAG     | GGGAT   | TATTCAM | TCC    | TACAG  | CA     | 300   |     |      |      |
| Db | 1192 | CAAT   | GGGGGTT   | ATTAT - AT | GGATG    | AGCTTG   | GAGAG    | GGCTT     | CTCA    | AGAG    | AGAG   | AGCTT  | TC     | 1249  |     |      |      |
| OY | 301  | AAAG   | AGAGCT    | CGAGCT     | TATGG    | CGACAG   | ATG      | CTAAAC    | ATTG    | CTAA    | AGTAA  | AGTT   | ACT    | CCC   | 360 |      |      |
| Db | 1250 | GAGG   | CGAGAT    | GTGCT      | GTG      | SGAG     | AGAT     | CAAT      | CAAT    | CAAT    | GAAG   | TAA    | ACT    | AAAT  | GTG | CGCA | 1309 |
| OY | 361  | GGTTC  | TGTTGT    | ATAT       | GTAT     | TGA      | CCCCG    | GC        | TACT    | TAG     | CCCTG  | 404    |        |       |     |      |      |
| Db | 1310 | GGGG   | CGTCTG    | TTCAT      | TGCTCG   | AGG      | CGCAG    | GGTGG     | TTAG    | AG      | GTG    | 1353   |        |       |     |      |      |

## RESULT 9

AAT33139

AC AAT33139;

DT 07-DEC-1996 (first entry)

DE Broccoli ACC synthase cDNA clone TA13.

KW ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase;  
KW ethylene; shelf-life; *Cucumis melo*; melon; transgenic plant;  
KW antisense; broccoli; ss.

OS Brassica oleracea.

|  | Key | Location/Qualifiers |
|--|-----|---------------------|
|--|-----|---------------------|

ET

```
/*tag= b
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| FT | primer_bind | 975..993 |
|----|-------------|----------|
| FT | primer_bind | 975..993 |

/Note= "primer RMM491"

PN W09621027-A1.  
XY

11-JUL-1996  
PD  
XX

PE 07-JUN-1995; 95WC-050/211.  
XX  
XX

XX 30-DEC-1994; 3405-030099Z

[illegible][illegible]

DR P-PSDB; AAR98599.

PT DNA encoding 1-an

PT in plants, esp. to improve shelf life

PS Claim 3; Fig6A-C; 50pp; English.

CC *Brassicacicerale* cDNA clone TAI3 (AA733137) (codes for  
CC 1-aminocyclopropane-1-carboxylic acid synthase (ACC-synthase)  
CC (AA985599), an enzyme involved in ethylene biosynthesis. It was  
CC obtained by PCR amplification (see also AA733140) of broccoli (*Brassica  
CC oleracea*). The PCR product was cloned into pCRIT to obtain clone  
CC TAI1. cDNA or genomic DNA (see also AA733136) can be inserted,  
CC sense or antisense orientation, into an expression cassette and  
CC transferred to a binary vector suitable for *Agrobacterium*-mediated  
CC plant transformation. The constructs permit control of the level of  
CC ACC synthase in a transgenic plant (esp. *B. oleracea* or *Cucumis  
CC melo*) and hence a control of maturation, ageing and shelf-life.

Sequence 993 BP; 269 A; 233 C; 253 G; 238 T; 0 other;

|             |                                       |
|-------------|---------------------------------------|
| Query Match | 20.38; Score 82.2; DB 17; Length 993; |
|-------------|---------------------------------------|

Best Local Similarity 55.0%; Pred. No. 3.3e-18;  
Matches 203; Conservative 0; Mismatches 165

Matches 203; Conservative 0; Mismatches 163; Indels 3; Gaps 2;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | GGGTGGCGGGGTTCCAGAGATGGGGGTTATCTATACCTCCACAAACGGAAACGTCCTACT     | 60  |
| Db | 621 | GGCTTCCCGSTTTTCAGAGTTGGAGACATTACTCGTACAAACGATATATGTTGTGAGSACA    | 680 |
| QY | 61  | GCCAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGACGGCTTGCCTGCTT         | 120 |
| Db | 681 | GGCGAAAGAGTGTGAGATTTTCAGCTTGTCTCGCTGACACAAACATGTTGGCTTCC         | 740 |
| QY | 121 | ATGCTCTCGACACGCGGTTCCATCCAAAGTTCATCGAGGTAAACAGACGAAACTCAA        | 180 |
| Db | 741 | ATGTGTTCGATGATGAAGAGTTTACGCGAAGACTACTAATGATATTAACCGTGAAGGCTTAG   | 800 |
| QY | 181 | AGATGTACAGCTGTGATTCGAGGGCGGGGTTGAAGAACAATCGGCGATCGAGTACGACGGAAAG | 240 |
| Db | 801 | AGACGGTACCGACAAATTTGTGGAAAGGGCTT-AAAGAAAGCAGGATGACAGTGTTTGAAGGG  | 859 |
| QY | 241 | CAGCGGAGGCTTCTCTATTGTGTGGGCCGACATGACGGGATTTGAATTCGATCTTAACGGA    | 300 |
| Db | 860 | TAATGCAAGGGT--TGTTCTGTTGGATGAATTTGGGTTCTTGTCTGCACAGAAAGGAAA      | 917 |
| QY | 301 | AAAGAGACGCTCGAGCTATGAGGACAAGTTGCTTAACATTTCTTAAGGTAAACGTTACTCCC   | 360 |

```

Db      918 CAAAGCAGCTCGAGCTTTGGTGTGATCTCTGAGAGACTAAAGCTGAATATATCTCTCT 977
QY      361 GGTTCCTTGT 369
        |||
Db      978 GATCTTCGT 986

RESULT 10
AAT73502
ID      AAT73502 standard; cDNA to mRNA; 1868 BP.
XX
AC      AAT73502;
XX
DT      26-AUG-1997 (first entry)
XX
DE      Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS2.
XX
KM      Ozone; induction; exposure; resistance; transgenic plant; ACC;
XX      1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.
XX
OS      Poplar nigra.
XX
FH      Key Location/Qualifiers
FT      CDS 119..1579
FT      /*tag= a
FT      /product= PNACCS2

JP09075088-A.
XX
PD      25-MAR-1997.
XX
PF      07-SEP-1995; 95JP-0254510.
XX
PR      07-SEP-1995; 95JP-0254510.
XX
PA      (TOYT ) TOYOTA JIDOSHA KK.
XX
DR      WPI: 1997-239270/22.
DR      P-PSDB; AAW21755.
XX
PT      Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
PT      enzyme genes - from poplar tree, are useful for generating
PT      ozone-resistant trees and pollution clean-up trees
XX
PS      Claim 2; Pages 9-11; 12pp; Japanese.
XX
CC      This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-
CC      carboxylic acid (ACC) synthase gene isolated from poplar trees which
CC      had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC      for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
CC      humidity, 30 k lux and air current 30 cm/second. This gene will be
CC      useful for breeding air pollutant ozone-resistant trees, especially
CC      poplar.
XX
SQ      Sequence 1868 BP; 590 A; 366 C; 405 G; 507 T; 0 other;

Query Match 20.3%; Score 82; DB 18; Length 1868;
Best Local Similarity 53.5%; Pred. No. 5,4e-18;
Matches 216; Conservative 0; Mismatches 185; Indels 3; Gaps 2;

QY      1 GGGTGGCGGGGTTCAGAGATGGCGTTATCTACTACACAGAGAAAGTGTCTACTACT 60
        |||
Db      944 GGACTCCCTGGCTTCAGAGTTGGAATGTCTACTATACAAAGATGAGTTGTTATTC 1003
        |||

QY      61 GCCAAAAAGTTGACAGATTTTCATTCATTCCAGCTCCGACGACGCGCTTGCCTGCTT 120
        |||
Db      1004 GCGCGAAGAGTCAAGATTTTGGTCTCTCTCACAACTCAATATTACTTGTCTTCA 1063
        |||

QY      121 ATGCTTCGAGACGCGGTTTACTCAAAAAGTTTCATTCAGAGTAAACAGAGCAAACTCAA 180
        |||
Db      1064 ATGGTTTCTGTGAAGAGTTTGTCTGAGAGATTCTTAGCCGAGAGCTCGAAGAGGCTTAAAG 1123
        |||

QY      181 AGAATGATACGCTGATTCGTGGCGGGGTGTAAGAAACTCGCATTCGATGCACGGAAG 240

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Db      1124 AAAAGCAGCGGTATTTTCACAAAGGATTTGGAAACA- TTGGGATCAGTGTGTTGGAAG 1182
QY      241 CAGCGAGCGCTTCCTATATTTGGGCGACATGAGCGGATTCATCTACAGCGAA 300
        |||
Db      1183 CAAAGCCGG--TCTCTTTGTTGGATGAATTTGCCCATCTCCCTTAAGAAACAANAAT 1240
QY      301 AAAGAGAGCTCGAGCTATGAGGACAACTTGCTTAACAATTCGTAAAGTAAACGTTACTGCC 360
        |||
Db      1241 GATGGTGAATGGAACGTGGCGGTGTGATGCTTAATGACGTAAGCTAAATGTTTCGCCA 1300
QY      361 GGTTCCTTGTGTCAATTTGTAATGAACCCGCGTACTTGTAGCCCTCG 404
        |||
Db      1301 GGCCTTCCTTCATTCGCTTGAGACCTGGTTGTTAGGGGTCTG 1344

RESULT 11
AAT73501
ID      AAT73501 standard; cDNA to mRNA; 1864 BP.
XX
AC      AAT73501;
XX
DT      26-AUG-1997 (first entry)
XX
DE      Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS1.
XX
KM      Ozone; induction; exposure; resistance; transgenic plant; ACC1;
XX      1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.
XX
OS      Poplar nigra.
XX
FH      Key Location/Qualifiers
FT      CDS 194..1639
FT      /*tag= a
FT      /product= PNACCS1

JP09075088-A.
XX
PD      25-MAR-1997.
XX
PF      07-SEP-1995; 95JP-0254510.
XX
PR      07-SEP-1995; 95JP-0254510.
XX
PA      (TOYT ) TOYOTA JIDOSHA KK.
XX
DR      WPI: 1997-239270/22.
DR      P-PSDB; AAW21754.
XX
PT      Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
PT      enzyme genes - from poplar tree, are useful for generating
PT      ozone-resistant trees and pollution clean-up trees
XX
PS      Claim 2; Pages 7-9; 12pp; Japanese.
XX
CC      This sequence, designated PNACCS1, is a 1-aminocyclopropane-1-
CC      carboxylic acid (ACC) synthase gene isolated from poplar trees which
CC      had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC      for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
CC      humidity, 30 k lux and air current 30 cm/second. This gene will be
CC      useful for breeding air pollutant ozone-resistant trees, especially
CC      poplar.
XX
SQ      Sequence 1864 BP; 574 A; 360 C; 392 G; 538 T; 0 other;

Query Match 20.0%; Score 80.8; DB 18; Length 1864;
Best Local Similarity 50.0%; Pred. No. 1,4e-17;
Matches 202; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY      1 GGGTGGCGGGGTTCAGAGTGGCGTTATCTACTACACAGAGAGCTGTCTACTACT 60
        |||
Db      1025 GGCCTCCCTGGCTTCAGAGTTGGAATTCATTCCTTAACAATGATGAGTTGAGTTGC 1084

```



```
QY 61 GCCAAAAAGTTGACGAGATTTTCATTCACCTCCGACGCGCGCTTGTCTGCTG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1085 GCCCGCAGATGTCAGAGCTCGATTTGGTATCCACACAACCTAGTACCTAGACATCA 1144
QY 121 ATGCTCTGGACACGGGTTCACTCAAAAGTTATCGAGTAACAGACGAAACTCAAA 180
    ||||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||| |||
Db 1145 ATGCTATCGGATATGAATTTGTGGAGATGTTCTATTAGGGAAGCAAAAGAGATTAGCC 1204
QY 181 AGATGTAGACCTCATTTCTGGGGGGTTGAAGAAACCTGGCATCGATGACGGAAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1205 GCAGAGTATAGACTTTCACCTGAGCTTGATCAAGTACGATTTGTTGAAAGACA 1264
QY 241 CACGGGAGGCTCTCTATTGCTTGCGCCGACATGACGGGATTTGATTCCTACAGCGAA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1265 AGTATGCTGCGCTGTTTGTGGATGGATTTAGTAGACTCTCAACAGCAGACATTT 1324
QY 301 AAGGAGAGCTCGAGCTATGCGACAGTTGCTAAACATTGCTTAAGTAAACGTTACTCCC 360
    ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
Db 1325 AAGGCTGAATGGAAGCTATGCGGAGTTATATCATGAACTCAAGCTCAACGTTTCGCCG 1384
QY 361 GGTTCCTGTGTGATTTGATTTGAACCGGCTACTTTAGCCTCG 404
    ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
Db 1385 GGTTCCTGTGTGATTTGATTTGAACCGGCTACTTTAGCCTCG 1428
```

## RESULT 12

```
AAT72631
ID AAT72631 standard; DNA; 1096 BP.
```

```
XX AAT72631;
XX
XX 27-JAN-1998 (first entry)
```

```
DE Mangifera indica ACC synthase miacc1 gene.
```

```
XX ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
XX miacc1; ethylene biosynthesis; transgenic plant; senescence;
XX anti-sense expression system; plant development; fruit ripening;
XX EC 4.4.1.14; mango; multigene family; ss.
```

```
OS Mangifera indica.
```

```
XX Key Location/Qualifiers
XX CDS 1..1096
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FT /*tag= a
FT /product= miacc1
FT /EC_number= 4.4.1.14
FT /note= "sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."
```

```
XX MO9711166-A1.
```

```
XX 27-MAR-1997.
```

```
XX PF 20-SEP-1996; 96WO-AU00591;
```

```
XX PR 02-MAY-1996; 96AU-0009603.
```

```
XX PR 20-SEP-1995; 95AU-000559.
```

```
XX PA (UYOU ) UNIV QUEENSLAND.
```

```
XX OS Botella JR;
```

```
XX PI WPI, 1997-202875/18.
```

```
XX DR P-PSDB; AAW18289.
```

```
XX PT Pineapple, papaya and mango ACC synthase genes - used in gene
```

```
XX PT therapy to produce fruits with reduced senescence
```

```
XX PS Claim 4; Fig 4; 46pp; English.
```

```
XX CC This sequence represents a novel gene, miacc1, which is a member
```

```
CC of an ACC synthase multigene family found in mango. ACC synthase is
CC involved in the pathway for ethylene biosynthesis and the rate of
CC endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or anti-sense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.
```

```
XX Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;
```

```
QY Query Match 19.9%; Score 80.4; DB 18; Length 1096;
```

```
Db Best Local Similarity 53.2%; Pred. No. 1,5e-17;
```

```
Matches 215; Conservative 0; Mismatches 186; Indels 3; Gaps 2;
```

```
QY 1 GGGTTGCGGGGGTTGACGATGGCGGTTATCTACTCTACAAAGAGAGAGCTGCTCACT 60
```

```
Db 688 GGCCTCCCTGGCTTAAAGGTTGGCATGTTATCTATATAGATGATGATGATGATGAT 747
```

```
QY 61 GCCAAAAAGTTGACGAGATTTTCACTTTCAGCTCCGACGCGCTGCTGCTG 120
```

```
Db 748 ATCCGCAAGATGTCACAGCTTCGTTTGTAATCTCAACAACTCAATATTACTGCTTCA 807
```

```
QY 121 ATGCTCTGGACACGGGCTTCACTCAAAAGTTATCGAGTAACAGGGAACCTCAA 180
```

```
Db 808 ATGCTTCTGTATGATGATTTGTGGAGATTTGTACGGAAGCTCAAAAGGCTGGCA 867
```

```
QY 181 AGATGTAGACCTCATTTCTGGCGGGGTTGAAGAAACCTCGATCCAGTACGGAAG 240
```

```
Db 868 AAAAGGTACCATATTTTACAAAGAGACTTG-AAAAAGTGGGATTAACGCTTGAAGGG 926
```

```
QY 241 CACGGGAGGCTTCTCTATTGTTGGCCGACATGACGGGATTTGATTCATCTACAGGAA 300
```

```
Db 927 AAATGCAAG--TCCTTCTCTGTGATGATTTGGACACCTCCCTCAACAAAGACGTT 984
```

```
QY 301 AAGGAGAGCTCGAGCTATGCGAGCAAGTGTCTAACAATGCTTAAGTAAGGATCTGCC 360
```

```
Db 985 GATGCCGAATGAAGCTATATGGGCGACGATTTTGACCATGTGAAGACTTAAAGCTTCA 1044
```

```
QY 361 GGTTCCTGTGTGATTTGATTTGAACCGGCTACTTTAGCCTCG 404
```

```
Db 1045 GGTTCCTGTGTGATTTGATTTGAACCGGCTACTTTAGCCTCG 1088
```

## RESULT 13

```
AAT72632
ID AAT72632 standard; DNA; 1113 BP.
```

```
XX AAT72632;
```

```
XX 27-JAN-1998 (first entry)
```

```
DE Mangifera indica ACC synthase miacc2 gene.
```

```
XX ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
```

```
XX miacc2; ethylene biosynthesis; transgenic plant; senescence;
```

```
XX anti-sense expression system; plant development; fruit ripening;
```

```
XX EC 4.4.1.14; mango; multigene family; ss.
```

```
XX OS Mangifera indica.
```

```
XX PI WPI, 1997-202875/18.
```

```
XX DR P-PSDB; AAW18289.
```

```
XX PT Pineapple, papaya and mango ACC synthase genes - used in gene
```

```
XX PT therapy to produce fruits with reduced senescence
```

```
XX PS Claim 4; Fig 4; 46pp; English.
```

```
XX CC This sequence represents a novel gene, miacc1, which is a member
```

XX 27-MAR-1997.  
PD 20-SEP-1996; 96WO-AU00591.  
XX 02-MAY-1996; 96AU-0009603.  
XX 20-SEP-1995; 95AU-0005559.  
XX (UYOU ) UNIV QUEENSLAND.  
XX Botella JR;  
XX WPI: 1997-202875/18.  
DR P-PSDB; AAM18290.  
XX Pineapple, papaya and mango ACC synthase genes - used in gene  
PT therapy to produce fruits with reduced senescence  
XX  
PS Claim 5; Fig 5; 46pp; English.  
XX This sequence represents the novel gene, miacc2, which is a member  
CC of the mango ACC synthase multigene family. ACC synthase an enzyme  
CC involved in the pathway for ethylene biosynthesis and the rate of  
CC endogenous expression of ACC synthase is considered to limit  
CC substantially the rate of ethylene production. Endogenous ethylene is  
CC often deleterious to crops, especially if some form of mechanical  
CC wounding has occurred and diminishes their post harvest quality and  
CC storage life. Novel ACC synthase genes expressed in transgenic plants  
CC using either sense or antisense expression system may be used to control  
CC the regulation of plant development, in particular fruit ripening,  
CC reducing senescence and thus improving storage life.  
XX  
SQ Sequence 1113 BP; 320 A; 212 C; 264 G; 317 T; 0 other;

Query Match 19.9%; Score 80.4; DB 18; Length 1113;  
Best Local Similarity 53.2%; Pred. No. 1.5e-17;  
Matches 215; Conservative 0; Mismatches 186; Indels 3; Gaps 2;

OY 1 GGGTGGCGGGGTTGAGATGGGGGCTTATCTCTCAACGAGAGAGCTGCTACTACT 60  
DB 6G4 GGGTCCCAAGGCTTTAGGCTCGCATTTATCTATCATACAGATACAGTTGTGAGTTGC 753  
OY 61 GCCAAAAGTTGACGAGATTTTTCATCTTCAGCTCGACGACGCGTTGCTCGTCT 120  
DB 754 GCCTCAAAATGTCAAGCTTTGACTTGTATCATCAACAACTCAACATTATTCGCTTCA 813  
OY 121 ATGCTCTGGACACGCGGTTCACTCAAAAAGTTCAATCGAGGTAAACAGAGCAAACTCAA 180  
DB 814 ATGTATCATGATGATGATTTGTGTGGATAGTTCACTTACTGAGAGCTTAAAGGCTTGCA 873  
OY 181 AGAATGTACGCTGCATTTGCTGGCGGGGTTGAAGAACTCGGCATCCGATCGAGGAAAG 240  
DB 874 AAAAGGACAGAGCCCTTC-ACATGGGGCTATCTCAAGTAGGCAATTTGTTTAAAGG 932  
OY 241 CAGCGAGGCTTCTCTATTTGTTGGCCGACATAGCGGATTTGATTCCTACAGCGNA 300  
DB 933 CAATCGGGG--GCTATTTTTCGATGATTTGATTCATCTTCCTCAAGAGCAAACTGAT 990  
OY 301 AAAGAGAGCTCGACCTTATGGACAAAGTTGCTAAACATTGCTAAGGTAAAGCTTACTGCC 360  
DB 991 GAAGGAGGATGAAGAACTGTGAAGTGAATCAACGAAGTAAATTAATTTTCTCCG 1050  
OY 361 GGTCTGTGTGATGATTTGAACCGGCTACTTTAGCGCTG 404  
DB 1051 GGTTCCTCTTCAATGGCGCTAATCCAGAGTGCTTGGGTTTG 1094

RESULT 14  
ID AAX27501  
XX AAX27501 standard; cDNA; 1712 BP.  
AC AAX27501;  
XX

DT 26-MAY-1999 (first entry)  
XX Banana 1-aminocyclopropane-1-carboxylic acid synthase (ACS) cDNA.  
DE 1-aminocyclopropane-1-carboxylic acid synthase; ACS; EFE; banana;  
XX ethylene forming enzyme; ethylene biosynthesis; plant; fruit ripening;  
KW transgenic; enzyme; inhibition; flavour; texture; ss.  
XX  
XX Musa sp.  
XX US5886164-A.  
XX 23-MAR-1999.  
PD 15-APR-1996; 96US-0632598.  
XX 15-APR-1996; 96US-0632598.  
XX 15-APR-1996; 96US-0632598.  
XX (ZENE ) ZENECA LTD.  
XX Bird CR, Fletcher JD;  
XX WPI: 1999-228611/19.  
DR  
XX Novel isolated cDNA molecules ((pASC6) and (pACOS7)) encoding  
PT 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene  
PT forming enzyme (EFE) - useful for modifying fruit ripening  
XX characteristics, especially in bananas  
XX  
PS Claim 1; Columns 11-14; 22pp; English.  
XX

CC The invention relates to two isolated cDNA molecules ((pASC6) and  
CC (pACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS)  
CC and an ethylene forming enzyme (EFE), respectively. The clones are  
CC deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814,  
CC respectively. pASC6 and pACOS7 may be used to genetically control  
CC ethylene biosynthesis in plants and hence regulate the ethylene-induced  
CC processes involved in fruit ripening (and other ethylene related  
CC processes). Vectors comprising the cDNA sequences may be used to produce  
CC transgenic bananas with altered fruit ripening characteristics. The  
CC orientation of the pASC6 and pACOS7 used in the construct, will determine  
CC how the ripening process is affected. If the genes have a sense  
CC orientation, and transcribe mRNA that encodes an active enzyme, the rate  
CC of ripening will be increased (up-regulation) (however, full-length sense  
CC constructs can also be used to inhibit enzyme expression by co-  
CC inhibition). If genes encode antisense mRNA, they will inhibit the  
CC expression of the genes involved in fruit ripening and hence slow the  
CC process down (down-regulation). In this manner different spatial and  
CC temporal patterns of genes expression can be produced. Retardation of the  
CC rate of ripening will reduce the rate of deterioration of banana fruit  
CC after harvest. This helps in production of high quality fruit that has  
CC improved flavour and texture. The present sequence represents the cDNA  
CC sequence of the banana ACS enzyme.  
XX

SQ Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

Query Match 19.5%; Score 78.8; DB 20; Length 1712;  
Best Local Similarity 53.0%; Pred. No. 6.9e-17;  
Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;

OY 1 GGGTGGCGGGGTTGAGATGGGGGCTTATCTCTCAACGAGAGAGCTGCTACTACT 60  
DB 865 GGGCGTCCCTGGGTTCCGGCTGCGCTCATATATCTCTCAACGAGAGCGCGTGTACGCTGC 924  
OY 61 GCCAAAAGTTGACGAGATTTTTCATCTTCAGCTCCGACGACGCGTGGCTGCTGCT 120  
DB 925 GCGAGAGAGATGTGAGCTTGGACTGCTCTGCGACGACGACGCTCTGCTGCTTCC 984  
OY 121 ATGCTCTGGACACGCGGTTCACTCAAAAAGTTCAATCGAGGTAAACAGAGCAAACTCAA 180  
DB 985 ATGTTGGAGAGGAGAGATTCAACCGAGTTTCTTAGGACGACGCGGAGGTTTGTC 1044  
OY 181 AGAATGTACGCTGCATTTGCTGGCGGGGTTGAAGAACTCGGCATTCGATCGAGGAAAG 240

Db 1045 GGGCGGCCAGGCTTTACGG-ACGGCCTCAGCGAGTCGGGATTCTATTCCTGGACGG 1103  
QY 241 CAGCGGAGGCTTCTATTTGTTGGCCGACATGAGCGGATTCGATTCCTACAGCGAA 300  
Db 1104 CAAGCGGGG--GCTGTCTCTGATGAGCTTGAAGCCGCTGCTGAAGAGCGACGGTG 1161  
QY 301 AAAGAGAGCTCGAGCTATGGGACAACTTCTAAACATTCCTAAGTTAAAGTTACTCC 360  
Db 1162 GAGCGGAGCTCCGCTGTCGGGTGATCATCAACGACGAGCTCAACATCTCCGGC 1221  
QY 361 GGTCTTGTGTCATTTGATTTGAACCCGGCTACTTTAGCCTCTG 404  
Db 1222 GGGTCGCTTCCACTGCTCGAGCCGGGGTGTTCAAGGGTGTG 1265

RESULT 15  
AAS09901  
ID AAS09901 standard; cDNA; 1712 BP.  
XX  
AC AAS09901;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE DNA encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS).  
XX  
KW 1-aminocyclopropane-1-carboxylic acid synthase; ACS; banana;  
KM ethylene biosynthesis; ethylene-forming enzyme; EFE; fruit ripening;  
XX fruit storage; ss.  
OS Musa sp.  
XX  
XX  
PN US6262346-B1.  
XX  
PD 17-JUL-2001.  
XX  
PF 15-JAN-1999; 9905-0231240.  
XX  
PR 15-APR-1996; 9605-0632598.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Bird CR, Fletcher JD;  
XX  
DR WPI; 2001-450497/48.  
XX  
XX  
PT Modifying level of ethylene biosynthesis in plant of genus Musa,  
PT involves inserting into genome of plant a DNA sequence encoding banana  
PT 1-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming  
PT enzyme -  
XX  
XX  
PS Claim 2; Column 13; 23p; English.  
XX  
XX  
CC The sequence represents the coding sequence of 1-aminocyclopropane-1-  
CC carboxylic acid synthase (ACS) from banana, used in the method of  
CC the invention. The method involves modifying the level of ethylene  
CC biosynthesis in a plant of the genus Musa by inserting into the genome of  
CC the plant a DNA sequence (I) encoding a banana 1-aminocyclopropane-1-  
CC carboxylic acid synthase (ACS) or an ethylene-forming enzyme (EFE), where  
CC (I) is in sense or antisense configuration, and modifies the level of  
CC activity of ACS or EFE. This retards the rate of ripening in banana  
CC fruits which reduces the rate of deterioration of banana fruit after  
CC harvest. As a result, fruit may be harvested when they have reached  
CC partial or full ripeness and still have the robustness to withstand  
CC handling and transport to reach the consumer in good condition. In this  
CC way high quality ripe fruit can be made available to the consumer with  
CC reduced requirement for post-harvest treatment. High quality fruit will  
CC have improved flavour and texture. High quality fruit can be produced  
CC consistently over a wide harvest period, and such fruit can be held in  
CC store for long periods and ripened to optimal quality by the supply of  
CC exogenous ethylene.  
XX  
SQ Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

Query Match 19.5%; Score 78.8; DB 22; Length 1712;  
Best Local Similarity 53.0%; Pred. No. 6.9e-17;  
Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;  
QY 1 GGGTTGCCGGGGTTACAGATGGCGCTTATCTACTCTTCAACAGAGAACGTCTCACTACT 60  
Db 865 GGGCTCCCTGGCTTCCGGGTCCATATATCTTCAACAGAGAACGTCTCACTACT 924  
QY 61 GCCAAAAGTTGACGAGATTTTCATTCATTCAGTCCGAGCGAGCGGCTTGTCTGCTT 120  
Db 925 GCGAGAGAGATGTGAGCTTTGGACTGCTCTGTCGACAGCGAGCTCTGCTGCTTCC 984  
QY 121 ATGCTTCGACACGCGGCTTCACCTCAAAAGTTTCATTCGAGTAAACAGAGCAAACTCAA 180  
Db 985 ATGTTGGAGACGAGAGATTCACCCAGAGTTCTTAGGAGAGAGCGGACGAGTTTGTGC 1044  
QY 181 AGAATGTACGCTGCATTCGTGCGGGGTTGANAAGAACTCGGATCGATCGACGGAAG 240  
Db 1045 GGGGGGCGCAGGGGCTTTACGG-ACGGCCTCAAGCGAGCTGGGATTCATTCCTTGACGG 1103  
QY 241 CAGCGGAGGCTTCTCTATTTGTTGGCCGACATGAGCGGATTCGATTCCTACAGCGAA 300  
Db 1104 CAAGCGGGG--GCTGTCTCTGATGAGCTTGAAGCCGCTGCTGAAGAGAGCGACGGTG 1161  
QY 301 AAAGAGAGCTCGAGCTATGGGACAACTTCTAAACATTCCTAAGTTAAAGTTACTCC 360  
Db 1162 GAGCGGAGCTCCGCTGTCGGGTGATCATCAACGACGAGCTCAACATCTCCGGC 1221  
QY 361 GGTCTTGTGTCATTTGATTTGAACCCGGCTACTTTAGCCTCTG 404  
Db 1222 GGGTCGCTTCCACTGCTCGAGCCGGGGTGTTCAAGGGTGTG 1265

Search completed: March 11, 2003, 00:52:07  
Job time : 181 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:47:37 ; Search time 1609 seconds

(without alignments)  
7307.355 Million cell updates/sec

Title: us-09-975-842-1

Perfect score: 404  
Sequence: 1 ggggtgcgggggttcagat.....cccgctacttaagctctcg 404

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rdg:\*  
36: em\_htg\_mar:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID         | Description         |
|------------|-------|-------------|--------|----|------------|---------------------|
| 1          | 196.4 | 48.6        | 894    | 8  | AF184076   | AF184076 Prunus ar  |
| 2          | 178   | 44.1        | 581    | 8  | AF146028   | AF146028 Actinidia  |
| 3          | 147.8 | 36.6        | 1674   | 8  | AF348575   | AF348575 Arabidops  |
| 4          | 147.8 | 36.6        | 1757   | 8  | AY054691   | AY054691 Arabidops  |
| 5          | 147.8 | 36.6        | 98412  | 8  | F16P17     | AC011000 Sequence   |
| 6          | 146.8 | 36.3        | 1089   | 8  | TAU35779   | U35779 Trilicium ae |
| 7          | 144.2 | 35.7        | 143113 | 8  | AP000559   | AP000559 Oryza sat  |
| 8          | 127.6 | 31.6        | 1468   | 8  | AF336920   | AF336920 Arabidops  |
| 9          | 127.6 | 31.6        | 86212  | 8  | AB010074   | AB010074 Arabidops  |
| 10         | 117.2 | 29.0        | 1372   | 8  | MSBACS2GE  | X96947 Musa acumina |
| 11         | 114   | 28.2        | 1812   | 8  | MSBACS1GE  | X96946 M.acuminata  |
| 12         | 110.8 | 27.4        | 1400   | 8  | AF312737   | AF312737 Malus x d  |
| 13         | 110.8 | 27.4        | 1618   | 8  | MSU03294   | U03294 Malus syive  |
| 14         | 110.8 | 27.4        | 1633   | 8  | MD0011518  | AJ011518 Malus dom  |
| 15         | 110.8 | 27.4        | 1778   | 8  | AB015624   | AB015624 Pyrus pyr  |
| 16         | 110.8 | 27.4        | 1812   | 8  | PCPCACSIG  | X87112 P.communis   |
| 17         | 110.8 | 27.4        | 2004   | 8  | MAUACCSYN  | L31347 Malus domes  |
| 18         | 110.8 | 27.4        | 5526   | 8  | MDU89156   | U89156 Malus domes  |
| 19         | 109.2 | 27.0        | 1840   | 8  | VRU34987   | U34987 Vigna radia  |
| 20         | 109.2 | 27.0        | 4405   | 8  | AF151961   | AF151961 Vigna rad  |
| 21         | 107.6 | 26.6        | 1344   | 8  | AF332390   | AF332390 Arabidops  |
| 22         | 107.6 | 26.6        | 5676   | 8  | AB010102   | AB010102 Malus dom  |
| 23         | 107.6 | 26.6        | 89904  | 8  | ATTC5K17   | AL049171 Arabidops  |
| 24         | 107.6 | 26.6        | 196286 | 8  | ATCHRIV64  | AL161564 Arabidops  |
| 25         | 106   | 26.2        | 3758   | 8  | AF049711   | AF049711 Petunia x  |
| 26         | 104.8 | 25.9        | 1413   | 8  | AF334720   | AF334720 Arabidops  |
| 27         | 104.8 | 25.9        | 1413   | 8  | AFTHACS58  | L29261 Arabidops    |
| 28         | 104.8 | 25.9        | 1873   | 8  | AB000679   | AB000679 Vigna rad  |
| 29         | 104.8 | 25.9        | 1892   | 8  | VRU34986   | U34986 Vigna radia  |
| 30         | 104.8 | 25.9        | 3234   | 8  | NTA131837  | AJ131837 Nicotiana  |
| 31         | 104.8 | 25.9        | 4284   | 8  | ATTHACSSA  | L29260 Arabidops    |
| 32         | 104.8 | 25.9        | 4714   | 8  | AB018355   | AB018355 Vigna rad  |
| 33         | 104.8 | 25.9        | 84440  | 8  | AB010075   | AB010075 Arabidops  |
| 34         | 104.8 | 25.9        | 118086 | 8  | ATFEH11    | AL021684 Arabidops  |
| 35         | 103   | 25.5        | 1089   | 8  | AB021908   | AB021908 Musa acum  |
| 36         | 102.8 | 25.4        | 1410   | 8  | AF334712   | AF334712 Arabidops  |
| 37         | 102.8 | 25.4        | 1413   | 8  | AF332391   | AF332391 Arabidops  |
| 38         | 102.8 | 25.4        | 1638   | 8  | CUCACCA    | D01033 Cucurbita m  |
| 39         | 102.8 | 25.4        | 4346   | 8  | CM037774   | U37774 Cucurbita m  |
| 40         | 102.8 | 25.4        | 97711  | 8  | ATT16K5    | AL132965 Arabidops  |
| 41         | 102.8 | 25.4        | 110766 | 8  | ATT28119   | AL035709 Arabidops  |
| 42         | 102.8 | 25.4        | 198493 | 8  | ATCHRIV88  | AL161592 Arabidops  |
| 43         | 101.2 | 25.0        | 1115   | 8  | AF338651   | AF338651 Brassica   |
| 44         | 101.2 | 25.0        | 1393   | 8  | VIRACCSYNT | M94863 Vigna radia  |
| 45         | 101.2 | 25.0        | 1393   | 8  | VRACCSYNS  | Z12134 V.radiata g  |

#### ALIGNMENTS

RESULT 1  
AF184076 LOCUS 894 bp DNA linear PLN 01-OCT-2000  
DEFINITION Prunus armeniaca ACC synthase (ACS1) gene, partial cds.  
ACCESSION AF184076  
VERSION AF184076.1 GI:10441264  
KEYWORDS  
SOURCE  
ORGANISM Prunus armeniaca.  
Prunus armeniaca  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.  
REFERENCE  
1 (bases 1 to 894)  
Mbeguile-A-Mbeguile,D. and Fils-Lycaon,B.R.  
Molecular cloning and nucleotide sequence of genomic DNA encoding

Pred. No. is the number of results predicted by chance to have a

| JOURNAL                                      | REFERENCE  | AUTHORS   | TITLE    | JOURNAL         | FEATURES |
|--|--|---|----------|-----------------|----------|
| ACC synthase from apricot fruit              | Unpublished  | 2 (bases 1 to 894)  |          |                 |          |
| Mbeguile-A-Mbeguile, D. and Fils-Lycan, B.R. | Submitted (07-SEP-1999)  | Station de Technologie des Produits Vegetaux, Institut National de la Recherche Agronomique, Agroparc-Domaine Saint Paul, Avignon 84914, France |          |                 |          |
| location/Qualifiers                          |  |   |          |                 |          |
| source                                       |  |   |          |                 |          |
| gene   |  |   |          |                 |          |
| mRNA   |  |   |          |                 |          |
| CDS  |  |   |          |                 |          |
| BASE COUNT                                   |  |   |          |                 |          |
| ORIGIN                                       |  |   |          |                 |          |
| Query Match                                  | 48.6%  | Score 196.4   | DB 8     | Length 894      |          |
| Best Local Similarity                        | 71.5%  | Pred. No. 1.2e-51   |          |                 |          |
| Matches 286                                  | Conservative 0   | Mismatches 111  | Indels 3 | Gaps 2          |          |
| 5  | TCGCGGCTTCAGATGGGCGTTATCTACTCTACACAGACAGTGTCTACTACTGCA           | 64  |          |                 |          |
| 497  | TTCCAGGTTTAAAGCGGGGTGTATCTACTCTTTAAACAAATGTGCTGGCTCTGTA          | 556   |          |                 |          |
| 65   | AAAATTGACGAGATTTTCATCATCTTTAGCTCCGACGACGCGTTCCTGCTTATGC          | 124   |          |                 |          |
| 557  | AAAGTTAACAAAGTTCTCGTCATCTCCATCCCAACAGTGTCTCAGCTATGC              | 616   |          |                 |          |
| 125  | TCTCGACACGCGGTTCACTCAAAAGTTCATGAGGTAACAGACGCAACTCAAAAGAA         | 184   |          |                 |          |
| 617  | TTTCAGACACCAAAATTTTCCAAAAGTTTATGTAGTCCAAATGAGAGAGACTTCGAGAA      | 676   |          |                 |          |
| 185  | TGTACGCTGCATCTGCGGGGGGTGAAGAAATCGGCATCCGATCGACGGAAGCAGC          | 244   |          |                 |          |
| 677  | TTCACCTTAATTTCTGAC-AGGTTTGAAGCAATTTGGGCATTTGAGTGTACAAAGACAT      | 735   |          |                 |          |
| 245  | GGAGGCTTCTATTGTTGGGCGCATGAGCGGATTAATTCATGCTCAACGCAAAAG           | 304   |          |                 |          |
| 736  | GGAGG-TTTCAGCTGTTGGGACACATGAGTGGGTTATCCGCTTACATGGAAG             | 793   |          |                 |          |
| 305  | GAGACTGAGCTATGAGGACAGTTGCTAAACATTTGCTAAAGTAAAGTCTCCCGGT          | 364   |          |                 |          |
| 794  | GGGAGCTTGAAGCTGGGATGAGTTGTAAGTGAAGTAAATGTAATGTAATCTCCGGAT        | 853   |          |                 |          |
| 365  | CTTGTGTCATTGTTTGAACCCGGCTACTTATGACCTGTG                          | 404   |          |                 |          |
| 854  | CTTCATGTCATTTGTAATGAAACCCGGCTGTTCCGGTGTG                         | 893   |          |                 |          |
| RESULT 2                                     |  |   |          |                 |          |
| AF146028                                     | 581 bp   | DNA   | linear   | PLN 17-MAY-1999 |          |
| LOCUS  |  |   |          |                 |          |
| DEFINITION                                   | Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 3 |   |          |                 |          |
| ACCESSION                                    | AF146028   |   |          |                 |          |
| VERSION                                      | AF146028.1   | GI:4836802  |          |                 |          |
| KEYWORDS                                     |  |   |          |                 |          |

|                       |   |
|-----------------------|---|
| SOURCE                | Actinidia chinensis.  |
| ORGANISM              | Actinidia chinensis   |
| REFERENCE             | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae, Ericales; Actinidiaceae; Actinidia.  |
| AUTHORS               | Xu,C., Chen,K., Chen,D. and Zhang,S.  |
| TITLE                 | Molecular cloning of four members of ACC synthase gene family from kiwifruit (actinidia chinensis Planch.)  |
| JOURNAL               | unpublished   |
| ADTHORS               | 2. (bases 1 to 581)   |
| TITLE                 | Xu,C., Chen,D., Chen,K. and Zhang,S.  |
| JOURNAL               | Direct Submission<br>Submitted (27-APR-1999) Department of Horticulture, Huajiang Campus, Zhejiang University, Kaxianlu 268, Hangzhou, Zhejiang 310029, People's Republic of China  |
| FEATURES              | location/Qualifiers   |
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| BASE COUNT            | 166 a 112 c 132 g 171 t   |
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| Query Match           | 44.1%; Score 178; DB 8; Length 581;   |
| Best Local Similarity | 70.3%; Pred. No. 9e-46;   |
| Matches               | 267; Conservative 0; Mismatches 110; Indels 3; Gaps 2;  |
| OY                    | 10 GGTTCCAGATGGCGGTATCTACTCCACAAAGCAGTGCCTACTACTGCCAAAAG 69   |
| DB                    | 204 GGTTTCGGATGGGGATTATCTACTCTCTTCATGGAATGTACTGTCTGCTCCAAAAA 263  |
| OY                    | 70 TTGACGAGATTTCATTCATTTACCTTCACCTCCGAGCGACGCTTGCTGCTGTTATGCTCTCG 129   |
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| OY                    | 130 GACACGCGGTACTCCAAGAATTCATCGAGTAACGAAACAGGAAACCTAAAAGATGTAC 189  |
| DB                    | 324 GATACAAATTTTGTGATATAATTTTCAAGACAAATTCAGAAAGGCTCACCGGATTTGC 383  |
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| DB                    | 384 AGTGAATTTGTTG-TTGSGTTGAACGATTTAGGTATAGAAATCCGCAAAAACAAATGCGGG 442   |
| OY                    | 250 GTTCTCTATTTGTTGGCCGACATGAGCGGATTTGATTCATCTTAACGAAAAAGGAAAG 309  |
| DB                    | 443 --TTTCTATTTGTTGGGCTGCATCGGCTGGTGTGATCTCTCTCAATACGAGAGAAAGCGAG 500   |
| OY                    | 310 CTCGAGCTATTTGGGACAAAGTTGCTTAACATTTGTAAGTAACAGTACTCCGCTCTTGT 369   |
| DB                    | 501 CGAAACCTCTGGGATTAAGTTGTTGATGATGAGCTAAGGTTAATGTAACCTCGATCTTCC 560  |
| OY                    | 370 TGTCAATTTGATTGAACCCGG 389   |
| DB                    | 561 TGTCACTGTATTGAACCTGG 580  |
| RESULT 3              |   |
| LOCUS                 | AF348575 1674 bp mRNA linear PLN 18-APR-2002  |
| DEFINITION            | Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase ACS10 (At1g96260) mRNA, complete cds.   |
| ACCESSION             | AF348575  |

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VERSION AF348575.1 GI:13194767
KEYWORDS FL1.CDNA.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS 1 (bases 1 to 1674)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etyu,P.,
Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,
Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and
Theologis,A.
TITLE Arabidopsis Open Reading Frame (ORF) Clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1674)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Brooks,S.,
Chao,Q., Chen,H., Cheuk,R., Karlin-Neumann,G., Kim,C., Lam,B.,
Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
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Location/Qualifiers
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ecotype: Columbia"
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DELGNPDGVTQIGLAONNKISLDVWLENPKREKAIISDLSISGATSYPPSGILEKMA
VAGFMTKATNSVTEPDSQVLVTSGASSALEILSFLCJADSGMAFLVTPGSGIDROY
KMTGVDIHPVCRSADNENSMVWLDRAFYQARKRGVRIIGTIIISPSNMGSLSR
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SKDLSFRGSRSAITSENESVLSASRKLTLTPVSPSTOHLIIAISNPKVORFVKT
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BASE COUNT 443 a 343 c 403 g 485 t
ORIGIN
Query Match 36.5%; Score 147.8; DB 8; Length 1674;
Best Local Similarity 63.3%; Pred. No. 5,2e-36;
Matches 256; Conservative 0; Mismatches 142; Indels 3; Gaps 2;

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Db 1372 ATCTACAGGAGCTCGTG-AGGGGTTGAAGATTAGGAGTGCAGCAAGAACAA 1430
QY 244 CGAGAGCTTCTATTTGGGCCCCAGCAGCGGATGATTCATCCACGCAAAAA 303
Db 1431 TCGAAGGT-TCTACTGTTGGGCTGATATGCGAGGATGATTTCACTTACAGCAAAA 1488
QY 304 GGAGAGCTCGAGCTATGGGCAAGTTGCTAAACATTCCTAAACGTTACTCCCGGT 363
Db 1489 GCGAGATTGACCTGTGGACACAGCTTGACACATGGCAGATGCATGCACACAGA 1548
QY 364 TCTTGTGTCATGTTATTCAGACCCGGCTACTTTCAGCTCTG 404
Db 1549 TCTTGTGTCATGTTATTCAGACCCGGCTACTTTCAGCTCTG 1589

RESULT 4
AY054691
LOCUS 1757 bp mRNA linear PLN 05-SEP-2001
DEFINITION Arabidopsis thaliana strong similarity to ACS5 from lupinus albus
gb|AF119414, and contains an Amino transferase-class1 domain
pf100155 (At1g62960; F16P17.11) mRNA, complete cds.
ACCESSION AY054691 GI:15451221
VERSION AY054691.1
KEYWORDS
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS 1 (bases 1 to 1757)
Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carinici,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Marusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2001) DNA sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT e-mail for correspondence: arbd@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN
Arabidopsis Full-length cDNA"); Seki,M., Marusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carinici,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

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/db_xref="taxon:3702"
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DELGNPGVILQGLAONKSLSDMDVLENPEALSDGISIGIASYSPDGLILKMAA
VAGMTEATKNSYTSFVSQVLITGSGASAIIEELFPCLDASGNALVLPSPGSDYDRAV
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ENYALIDAFERENIHTISNIEFAGVSGEGRGVSMAEIVDTEENIDREWHIVYLD
SKDLSFGIRSAATKSYNESYLSKRLLTISPTVSTPHLLISAISPNKVOFFVT
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|-----------------------|-----------------|--------------------|-----------|--------------|
| Query Match           | 36.6%;          | Score 147.8;       | DB 8;     | Length 1757; |
| Best Local Similarity | 63.8%;          | Pred. No. 5.3e-36; |           |              |
| Matches 256;          | Conservative 0; | Mismatches 142;    | Indels 3; | Gaps 2;      |

Oy 4 TTGCGGGGTTCAGATGGCGTTATCTACTCTACAACGAGAAGTGCTCACTACGCC 63  
||| ||| | | | | | | | | | | | | | |  
Db 1230 TTCCGGGGCTTAGTCCCGTGCATTCTACCGTTCAACGAGAGTGTTTATCCGCTTCA 1289

Qy 64 AAAAAGTTACGAGATTTTCATTCCATTTCACTCCGACGCGGTGGTCTGTTATG 123  
+  
Db 1290 AGAAGCTCAGCGCTTCACCTGTCTCATNTCCAACCACAATTTTGCTGATATCCGA 1349

QY 124 CTCTCGGACACGGCGTTCTACTCMAAAGTTTCATCGAGGTAAACAGACGGAACCTCAAAAAGA 183  
||| | | ||| | | | ||| | | | |  
Db 1350 ATCTCCAAATCCAAAAAATGTTTCAGAGATTCTGAAAACCAACACGACAGAGATTTCACAGGT 1409

QY 184 ATGTACGCTGCATTCGTGGGGGGGGTGTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243  
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 Db 1410 ATCTACACGGAGCTCTGTG-AGGGGTGAAGAGATTAGGGATCGACTGCACCAAGAACGAA 1468

QY 244 CGGAGGCCTCTCATTGTGGGCCGACATGAGCGGATTGATTCGATCTCAAGCCAAAA 303  
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Db 1469 TGGAGGGT--TCTACTGTTGGGCTGATATGCGAGGATTGATTTCATCTTACACGAAAAA 1526

Qy 304 GGAGAGCTCGAGCTATGGGACAAGTTGCTAACAATTGCTAAGCTAAACGTTACTCCGGT 363  
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 Db 1527 GCGGAGATTGAGCTGTGGAACAAGCTCTTGAACAATTGGCAAGATCATGTTCATACCAAGA 1586

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| RESULT 5 |          |     |        |                |
|----------|----------|-----|--------|----------------|
| F16P17/c |          |     |        |                |
| LOCUS    |          |     |        |                |
| F16P17   | 98412 bp | DNA | 110000 | PM 13-TTN-2000 |

| ACCESSION  | DEFINITION   |
|------------|--|
| AC011000.3 | Sequence of BAC Fib5b7 from <i>Arabidopsis thaliana</i> chromosome 1, complete sequence. |
| AC011000   |  |
| AC011000.3 | GT-7109456   |
| AC011000   |  |
| AC011000.3 |  |

LEIWORDS  
SOURCE  
ORGANISM  
HTG.  
Arabidopsis thaliana.  
Arabidopsis thaliana  
Eukerwota: Viridiplantae: Streptophyta: Embryophyta: Tracheobryta:

REFERENCE  
AUTHORS  
Sakano, H., Liu, S.-X., Yu, G., Lee, J. M., Lenz, C., Pham, P., Tortum, M.

Chen, C., Caihu, J., Choi, E., Chung, B., Gonzalez, A., Hwang, B., Liu, A., Vaysberg, M., Altafi, H., Brooks, S., Buehler, E., Chao, Q., Conn, L., Conway, A.B., Hansen, N.F., Johnson-Hopson, C., Khan, S., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.T., Shinn, P.,

TITLE of BAC F16p17 from *Arabidopsis thaliana* chromosome 1  
 The sequence  
 Unpublished  
 SOUTHWICK, A., DAVIS, R.W., ECKER, J. R., FEDERSPIEL, N.A. and  
 THEOLOGIS, A.

REFERENCE  
AUTHORS  
Z (bases 1 to 98412)  
Theologis, A.

|           |  |
|-----------|--|
| TITLE     | Direct Submission  |
| JOURNAL   | Submitted (29-SEP-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA |
| REFERENCE | 3 (bases 1 to 98412)   |
| AUTHORS   | Theologis,A.   |
| TITLE     | Direct Submission  |
| JOURNAL   | Submitted (29-FEB-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA |
| REFERENCE | 4 (bases 1 to 98412)   |
| AUTHORS   | Theologis,A.   |
| TITLE     | Direct Submission  |
| JOURNAL   | Submitted (13-JUN-2000) Plant Gene Expression Center, 800 Buchanan St., Albany, CA 94710, USA    |
| COMMENT   | On Feb 29, 2000 this sequence version replaced at:6453845  |

The sequence is U126C.F01.1 from Adenovirus ChAdV.C8 chromosome 1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 10039 bp because we submit only the unique sequence of the clone.

However, in order to

about 100 bp, overlapping clones in the future, for creation of larger contigs. We provide small overlaps (200 bp) between overlapping submitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone

| FEATURES | Location/Qualifiers              |
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DVTYNILIGVFKCAGFLRAEDYIEMLCGIIIPSTVYNSMVDGCFCKNLEERQ

gene  
complement(10587, .12875)  
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/evidence=not_experimental
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| Source   | Organism  |
|--|---|
| Triticum aestivum.   | Triticum aestivum.  |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;                      | Poideae; Triticeae; Triticum.   |
| 1 (bases 1 to 1089)  | Subramaniam, K., Abbo, S., and Heng, P. P.  |
| Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression | Plant Mol. Biol. 31 (5), 1009-1020 (1996)   |
| 7/000913   | 843943  |
| (bases 1 to 1089)  | Subramaniam, K.   |
| Direct Submission  | Submitted (11-SEP-1995) Kuppusswamy Subramaniam, USDA-ARS, Beltsville Agricultural Research Center, Plant Molecular Biology Laboratory, Beltsville, MD 20705, USA   |
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| /db_xref="GI:1173638"  | /translation="MGLAENHLSDLVREWMEHBPAMPARGDEERDLITSLATYVQYVLGALIKMALAKFMKROIHESSVSFDSOMVTTSATPAMELISCIADPPAGFLVPSPYPAMDRIKWRGTIELIPVCBSIDNINISTALEIAYNAOKRGVRGVILSNPSNPTEFSVKOTLRDLPATRKNIHLISIEVFASCTSGFEVAEYNLEDPDRGNVHTIGLSKDLSLAGRVGYITSYNESIVAAKIAREFSVTPFOHLYAMLS DKQFISNLKYRRLKRAYNLDAALKOYGIECFKSSGGFYCWADMSKFIIRSYSEKGERRIMDRLEEARAKVNVTPEGSSCHCIEPGW" |
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| ORIGIN   |   |
| Query Match  | 36.3%; Score 146.8; DB 8; Length 1089;  |
| Best Local Similarity  | 64.8%; Pred. No. 1e-35;   |
| Matches 249; Conservative  | 0; Mismatches 132; Indels 3; Gaps 2;  |
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| DB   | 707 CAGGGTTTCGATCGGAGTCATATTTTGTAACAAGAAGCATTTGTGAAGCAGCGGCA 766  |
| OY   | 68 AGTTGACGAGATTTTTCATCCATTAGCTCGAGCAGAGCGCTTGCTGCTTATGCTCT 127   |
| DB   | 767 ACATTGCCGAGATTCATCTGTGTGCACCCGACCCAGCGCCTTCTTGTCGATGCTTT 826  |
| OY   | 128 CGGACGCGGTTCACTCTCTCTCAAAAGTTCATCGAGGTAACAGACGACCAACTCAAAAGATG 187  |
| DB   | 827 CGGACGAGAAGTTTATTCTCAATTTACCTGAAGATTAAACAGAGAGAGGCTGCCAAGCGCT 886   |
| OY   | 188 ACGCTCATCTCGCGCGGGGTTGAAGAAATCGGCATCCGATCGACGAGGAAGACGCGGA 247  |
| DB   | 887 ACAATTCGCTCTTG-AATCCTTTGAAGCAGGCGGCGATCGAATGCTTCAAGAGCAGCGGA 945  |
| OY   | 248 GGCTTCTCTATTTGTGGCGCGACATGAGGGAATTGATTCGATCCGTAACGCGAAAAAGAG 307  |
| DB   | 946 GGGT--TCTACTGCTGGGAGACATGAGCAAGTTATCCGGCTTACAGCGGAAAGAG 1003  |
| OY   | 308 AACTCGAGTATGGGACGAAGTGTCAAACATGTCAAAGGTAACGTTACTCCGGGTTCTT 367  |
| DB   | 1004 AACGCAAGGCTTTGGGACAGGCTGTTGGAGAGGACGAAGSTCAATGTCACACCCAGGTCAT 1063   |
| OY   | 368 GTTTCATTTGTTATGACCCGCGCT 391  |

| Db                | 1064  | CTTGCCATGCAWTCAGCGGGTT | 1087                       |
|-------------------|---|------------------------|----------------------------|
| RESULT 7          | AP000559  | 143113 bp              | DNA linear PLN 21-MAR-2002 |
| LOCUS             | AP000559  |                        |                            |
| DEFINITION        | Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, clone:P0493C11.   |                        |                            |
| ACCESSION         | AP000559  |                        |                            |
| VERSION           | AP000559.1  | GI:6006355             |                            |
| KEYWORDS          |   |                        |                            |
| SOURCE            |   |                        |                            |
| ORGANISM          | Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0493C11.   |                        |                            |
| REFERENCE AUTHORS | Oryza sativa (japonica cultivar-group)<br>Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;<br>Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;<br>Ehmerioideae; Oryzaceae; Oryza.   |                        |                            |
| REFERENCE TITLE   | Sasaki,T., Matsumoto,T. and Yamamoto,K.<br>Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0493C11<br>Published Only in Database (1999)  |                        |                            |
| JOURNAL REFERENCE | 2 (bases 1 to 143113)   |                        |                            |
| AUTHORS           | Sasaki,T., Matsumoto,T. and Yamamoto,K.   |                        |                            |
| TITLE             | Direct Submission   |                        |                            |
| JOURNAL           | Submitted (01-Oct-1999) Takuji Sasaki, National Institute of Agricultural Resources, Rice Genome Research Program; Kannonadai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan<br>(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)  |                        |                            |
| COMMENT           | The orientation of the sequence is from nt to Sp6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCAN.0, BLASTX2.0, BLASTY2.0 as well as SplicePredictor (October1998 version). The genomic sequence was searched against the non-redundant database NRP(PIR,SWISSPROT, GENEBP, PDB) from MAFI DNABank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NR with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no. and RGP clone ID.  |                        |                            |
| FEATURES          | Location/Qualifiers   |                        |                            |
| source            | 1..143113<br>/organism="Oryza sativa (japonica cultivar-group)"<br>/cultivar="Nipponbare"<br>/db_xref="taxon:39947"<br>/chromosome="6"<br>/clone="P0493C11"<br>join(40..126,585..819,1979..2001,2924..2946,3836..4073<br>/note="hypothetical protein"<br>/codon_start=1<br>/protein_id="BAA84786.1"<br>/db_xref="GI:6006356"<br>/translation="MTISGSANSAPLPGIMVTHLDIAISQCNENKRIAPFVLIRPMH<br>MAATPHTRYKKPLSLTVTAQYGISTSGGRSLSEHDSSRNQVNASVOELAMDERMRY<br>ACGCHFLPLAHRESAPTLISGSHCPVPNCNTQSSDPLRAISNANGLAIDLIISNV<br>FLAAKRREPNQEOHGSSNGVPMALOIDIHNGSSNLTSPE"<br>join(7961..8199,8666..8737,8962..9033,9134..9205,<br>9487..9558,9770..9841,9939..10010,10098..10169,<br>10254..10372,10440..10511,10637..10708,10792..10863,<br>10948..11019,11102..11173,11262..11333,11448..11519,<br>11611..11682,11795..11866,11963..12034,12124..12195,<br>12272..12353,12398..12515,12601..12732,12838..13176,<br>13259..13629,13761..14114)<br>/note="ESTS C22657(S0014),C22656(S0014) correspond to a<br>region of the predicted gene<br>similar to receptor protein kinase, ERECTA (AC004484)"<br>/codon_start=1<br>/protein_id="BAA84787.1"<br>/db_xref="GI:6006357"<br>/translation="MAAARAPLMMVVVVGAVAEAASGGGGGEGEKALMGVFA<br>GFGNANALVDMDGCDHCAMRVCTDNDSFAVALNLSUNLGEGETSPIGLELNQ<br>PFDLGNKRLTGQIPDEIGDCISLRKYDLDSGNLLYGDPIPSISLKQLEELLKNQGLT |                        |                            |



|    |       |   |       |
|----|-------|---|-------|
| OY | 128   | CGACACCGCGGTCTACCTAATAAAGTTCACGAGGTAAACAGCGCAACTCCAAAGGATGT     | 187   |
|    |       |   |       |
| Db | 34849 | CGGACCAAAAGTTATCTATTTCAATTACCTAAAGTTAATAGAGAGATTTGCCAAGATGT     | 34908 |
|    |       |   |       |
| OY | 188   | ACGCTGCATTTGTTGGCGGGGTTTAAAGAACTCCGCAATCCATGCACGGAAGCAGCGGA     | 247   |
|    |       |   |       |
| Db | 34909 | ACCAATTTGTTTGTG - ATGCTTTGGATCAAGTGGGAGATTGAGTGTCTACAAAGACGTGGA | 34967 |
|    |       |   |       |
| OY | 248   | GCGTTTCTATTTGTTGGGCCACATGAGCGGATGATTCCATCCTACAGCGCAAAAAGAG      | 307   |
|    |       |   |       |
| Db | 34968 | GGGT--TCTACTGCGGGCAACATGAGACAGTTTCATCAGGCTTTACGCGCAAGAGGGG      | 35025 |
|    |       |   |       |
| OY | 308   | AGCTCGACCTATGGGACAGTGTGCTAAACATTTGCTAAGGTAAAGCTTACCOCGGTCTT     | 367   |
|    |       |   |       |
| Db | 35026 | AGCGCAACCTTTGGGATGATGATTTGGAGGAGGCAAGAGTCATATGTCACTCCAGTTTCAT   | 35085 |
|    |       |   |       |
| OY | 368   | GTTGTCATTGTATTTAACCOCGGCTACTTTAG                                | 398   |
|    |       |   |       |
| Db | 35086 | CTTGGCATTGCATCGAGCCTCGATGGTTACG                                 | 35116 |

| LOCUS      | 20  | 1488 bp   | mRNA | linear | PLN 18-APR-2002 |
|------------|---|---|------|--------|-----------------|
| DEFINITION | AF336920  | Arabidopsis thaliana l-aminocyclopropane-1-carboxylate synthase |      |        |                 |
| ACCESSION  | AF336920  | ACS12 (At5g51690) mRNA, complete cds.                           |      |        |                 |
| VERSION    | AF336920.1  | GI:12484204   |      |        |                 |
| KEYWORDS   | FLI cDNA.   |   |      |        |                 |
| SOURCE     | Arabidopsis thaliana.   |   |      |        |                 |
| ORGANISM   | Arabidopsis thaliana.   |   |      |        |                 |
| REFERENCE  | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.   |   |      |        |                 |
| AUTHORS    | 1 (bases 1 to 1488)   |   |      |        |                 |
| REFERENCE  | Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P., Lee,J.H., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H., Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.         |   |      |        |                 |
| JOURNAL    | Arabidopsis Open Reading Frame (ORF) Clones   |   |      |        |                 |
| REFERENCE  | Unpublished   |   |      |        |                 |
| AUTHORS    | 2 (bases 1 to 1488)   |   |      |        |                 |
| TITLE      | Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H., Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A. |   |      |        |                 |
| JOURNAL    | Direct Submission   |   |      |        |                 |
| REFERENCE  | Submitted (17-JAN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  |   |      |        |                 |
| AUTHORS    | Location/Qualifiers   |   |      |        |                 |
| FEATURES   | 1..1488   |   |      |        |                 |
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|            | /chromosome="5"   |   |      |        |                 |
|            | /clone="C00056"   |   |      |        |                 |
|            | /note="This clone is in pUNI-T3-D/V5-His-TOPO.  |   |      |        |                 |
|            | ecotype: Columbia"  |   |      |        |                 |
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|            | /note="ACC synthase"  |   |      |        |                 |
|            | /codon_start=1  |   |      |        |                 |
|            | /product="l-aminocyclopropane-1-carboxylate synthase  |   |      |        |                 |
|            | ACS12"  |   |      |        |                 |
|            | /protein_id="ANG54001.1"  |   |      |        |                 |
|            | /db_xref="GI:12484205"  |   |      |        |                 |
|            | /translation="MRLIVPLRGVIGIGRGGLFVSGLLPCLLFYQLQLYLKRREPPSC  |   |      |        |                 |
|            | PTDTRFTRSRILFDGRNWSSEIMMSQSDGDEDISISIMYKFEQILRLRYA  |   |      |        |                 |
|            | DGIDLGAEFTICEDLDGRNWSSEIMMSQSDGDEDISISIMYKFEQILRLRYA  |   |      |        |                 |

|                           |        |                    |           |              |
|---------------------------|--------|--------------------|-----------|--------------|
| Query Match               | 31.6%  | Score 127.6;       | DB: 8;    | Length 1488; |
| Best Local Similarity     | 60.8%; | Pred. No. 1.6e-29; |           |              |
| Matches 243; Conservative | 0;     | Mismatches 134;    | Indels 3; | Gaps 2;      |

|    |      |  |      |
|----|------|--|------|
| QY | 5    | TCGCGGGGTTGAGATGGGCGTTATCTACCTCTACCAAGAAACCTGCTCATCTACGCA      | 64   |
| Db | 1013 | TTCTCGGTTTAAAGAGCTGAGTCACTCACTCTCTTTCATGAAGAGCTAGTAAATGCTGCA   | 1072 |
| QY | 65   | AAAAGTTGACAGATTTTTCATCATTCCAGCTCCGACGACGCGTTCGTCGTTATGC        | 124  |
| Db | 1073 | AGAAGCTGATGATGATTTTTCATCAGTCCGACGTTCTTATGTTTCAAGGATTACTTCTCTAC | 1132 |
| QY | 125  | TCTCGGACACCGCGGTTCACCTCAAAAGTTCATCGAGGTAACGAGACGAAACTCAAAAGA   | 184  |
| Db | 1133 | TATCTGATGTAAGATTTCAATTAGGGGATCACTGCGACACACGCAAAAGATCCGGATA     | 1192 |
| QY | 185  | TGTACGCTGCATTCGTCGGGCGGTGGAAGAACTCGGCATCCGATGACGGAAGACAGC      | 244  |
| Db | 1193 | AGCATATTGCGTTTGTGG-AAAGTTTGAAACATTAGGAAATCCATGTGCTGAGAGTGT     | 1251 |
| QY | 245  | GGAGGCTTCTCATTTGTTGGGCGGCACATGAGCGGATTAATTCGATCTCAAGCGAAAAAG   | 304  |
| Db | 1252 | GGTGGGT--TGTATTTGTTGGGTAGACATGAGCAGTTTACTGACATCTTAAGTAGAAAG    | 1309 |
| QY | 305  | GAGAGCTCGAGCTATGSGACAATTGCTAAACATTGCTAAGCTAAACGTTACTCCCGTT     | 364  |
| Db | 1310 | GAGAACTCGAGTATTATTTAGAAAGCTATTGACTGTGCTAAAGATTAATGCACCTCCAGAA  | 1369 |
| QY | 365  | CTTGTGTCATTTGTAATTGAACCGCGCTACTTAAGCCTCG                       | 404  |
| Db | 1370 | CAGCCTGTTATTTAGAACCCAGGTTGTTAGGTGCTG                           | 1409 |

| RESULT 9   |   |
|------------|---|
| LOCUS      | AB010074/c  |
| DEFINITION | Arabidopsis thaliana genomic DNA, chromosome 5, PL clone:MI024.   |
| ACCESSION  | AB010074 BA0000015  |
| VERSION    | AB010074.2  |
| KEYWORDS   | GI:10177866   |
| SOURCE     |   |
| ORGANISM   | Arabidopsis thaliana (strain:Columbia) DNA, clone_1lib:MI024.   |
| REFERENCE  | Arabidopsis thaliana  |
| AUTHORS    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. |
| TITLE      | 1 (sites)   |
| JOURNAL    | Sato,S., Kaneko,T., Kotani,H., Nakamura,Y., Asamizu,E., Miyajima,N  |
| MEDLINE    | and Tabata,S.   |
| REFERENCE  | Structural analysis of Arabidopsis thaliana chromosome 5. IV.   |
| AUTHORS    | Sequence features of the regions of 1,456,315 bp covered by   |
| TITLE      | nineteen physically assigned P1 and TAC clones  |
| JOURNAL    | DNA Res. 5 (1), 41-54 (1998)  |
| MEDLINE    | 98290546  |
| REFERENCE  | 2 (bases 1 to 86212)  |
| AUTHORS    | Nakamura,Y.   |
| TITLE      | Direct Submission   |
| JOURNAL    | Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research  |
| MEDLINE    | Institute, Department of Plant Gene Research; 1532-3, Yana,   |
| REFERENCE  | Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,   |
| AUTHORS    | Tel:81-438-52-3935, Fax:81-438-52-3934)   |
| TITLE      | On Sep 15, 2000 this sequence version replaced gi:2760170.  |
| JOURNAL    | Address for correspondence: kaos@kazusa.or.jp   |
| MEDLINE    | For the latest information on annotation of this clone, please see  |
| REFERENCE  |   |

<http://www.kazusa.or.jp/kaos/cgi-bin/agd.graph.cgi?c=MIO24>  
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.  
The software programs used to predict genes include: Graal (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/Netgene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://greenlab.zool.iastate.edu/cgi-bin/sp.cgi>).  
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.  
The 5' clone is K10D11 and the 3' clone is MCM18.

## FEATURES

## source

1. 86212

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/strain="Columbia"

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## CDS

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IIVFAIGIVGICQPIYVGLAGISIGPGIKFISAMVOEYVAQGVLELFA  
LGLEFSTKLVGVGVVGLGLOIYVLMFGCVATLGCARISEGIVGAPFMSST  
AVVVKFVENSSTSLHGOVTGILIPDQVGLIFALLPVLGNSGLDGLISMKL  
LILSTLYTASLITNRFVPRPKIMQLSQRTRELIQIAVAFCLISANCSDKGLS  
LEISYVAGVWLSTTEPQHTLEQVLLNLSGRFCFASTCIGMLINHFVLMHVDILA  
SVLLIVIKTALAIAVAVKARYNMRISFHVGLAQIGERAFVLSRASNHVTEGRM  
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TLPTYSFKMLTKAEVGERALFIPKQGRDCTIIVKGYDSSLGENDLALALEHS  
PCGMISIRYFQTNDAEAVLKVHFIYMLQGTDEALKLNGSDMGCKLEVYDAERDF  
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## CDS

| Query Match  | Best Local Similarity  | 31.6%;     | Score 127.6;    | DB 8;     | Length 86212;   |
|--------------|--|------------|-----------------|-----------|-----------------|
| Matches 243; | Conservative   | 0;         | Mismatches 154; | Indels 3; | Gaps 2;         |
| QY 5         | TECCGGGCTTACAGATGGGCGCTTATCTCTCTCTACACGAGAACGCTGCTCACTACTGCCA 64   |            |                 |           |                 |
| Db 3393      | TTCCGCTTTTATAGACCTTGAGACATCTACTCTTTCATGAAAGCATAGTAATGGTGCA 3334  |            |                 |           |                 |
| QY 65        | AAAAGTTACGAGATTTTCATCTCATTTAGCTCCGACGAGCGGCTTGCCTCGCTTATGC 124   |            |                 |           |                 |
| Db 3333      | AGAACTATGATGATTTTTCATCAGTCCAGTCTTGATTCMAAGATACTTATCTCTTAC 3274   |            |                 |           |                 |
| QY 125       | TCTCGACACGCGGCTTCACTCAAAAAGTTCATCGAGGTAAACAGACGAGAACTCAAAAAGA 184  |            |                 |           |                 |
| Db 3273      | TATCTGATGTAAGATTTCACTTGAAGGATACATGCGACACAGGCAAGAGATCCGGGATA 3214   |            |                 |           |                 |
| QY 185       | TGTAGCTGCATTTCTGGGGGGGTTGAAGAAACCTCGATCCGATGCGAGAAAGCAGC 244   |            |                 |           |                 |
| Db 3213      | AGCAATTCGCTTTGTGC - AAGCTTTGAACAATTAAGAAATCCATGTCTCTAGAGTGGT 3155  |            |                 |           |                 |
| QY 245       | GGAGGCTTCTATTTGTTGGCGCATGAGCGGATTGATTGCATCTTACAGCGAAAAG 304  |            |                 |           |                 |
| Db 3154      | GCTGGGT - TGTATTTGGGTGATGACATGAGCAGTTTACTGCATCTTCACTGAGAAAG 3097   |            |                 |           |                 |
| QY 305       | GAGACTCGAGCTATGGACAAGTGTGAACATGTGTAAGTAAAGCTTACTCCGGTT 364   |            |                 |           |                 |
| Db 3096      | GAGAACTCGAGTTATTTGAAGACTATTGACTGTGTGCTAGATTATATGCACTCCAGGA 3037  |            |                 |           |                 |
| QY 365       | CTTGTGTCATTTGATTGAACCGGCTACTTAAAGCTCTG 404   |            |                 |           |                 |
| Db 3036      | CAGCCTGTTATTTGATTAAGAACACAGGTTGGTTCAAGGCTG 2997  |            |                 |           |                 |
| RESULT 10    | MSBACS2GE  | 1372 bp    | DNA             | linear    | PLN 01-MAR-2002 |
| LOCUS        | MSBACS2GE  |            |                 |           |                 |
| DEFINITION   | Musa acuminata bacs2 gene for 1-aminocyclopropane-1-carboxylate synthase.  |            |                 |           |                 |
| ACCESSION    | X96947   |            |                 |           |                 |
| VERSION      | X96947.1   | GI:1255948 |                 |           |                 |
| KEYWORDS     | 1-aminocyclopropane-1-carboxylate synthase; bacs2 gene.  |            |                 |           |                 |
| SOURCE       | Musa acuminata.  |            |                 |           |                 |
| ORGANISM     | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; Musa. |            |                 |           |                 |
| REFERENCE    | 1  |            |                 |           |                 |

|                           |   |
|---------------------------|---|
| AUTHORS                   | Liu,J. and Pua,E.   |
| JOURNL                    | Unpublished   |
| REFERENCE                 | 2 (bases 1 to 1372)   |
| AUTHORS                   | Liu,J.  |
| TITLE                     | Direct Submission   |
| JOURNAL                   | Submitted (27-MAR-1996) J. Liu, Department of Botany, National University of Singapore, Lower Kent Ridge Road, Singapore 119280,  |
| REPUBLIC OF SINGAPORE     |   |
| FEATURES                  | Location/Qualifiers   |
| SOURCE                    | 1..1372<br>/organism="Musa acuminata"<br>/cultivar="AAA group, cavendish"<br>/db_xref="taxon:4641"  |
| gene                      | 1..1372<br>/gene="bac2"<br>join(<1..21,110..241,327..487,589..> 372)<br>/gene="bac2"  |
| mRNA                      | /product="1-aminoacyclopropane-1-carboxylate synthase"<br>join(1..21,110..241,327..487,589..> 372)<br>/gene="bac2"  |
| CDS                       | /EC_number="4.4.1.14"<br>/codon_start=1<br>/product="1-aminoacyclopropane-1-carboxylate synthase"<br>/protein_id="CAA65648.1"<br>/db_xref="GI:1255949"<br>/db_xref="SPTRDBL:Q42924"<br>translation="MGLENQLIDLIEGGERHPDAVGLRDCALYSRELAFODYH<br>GLPGRKLADFMGELEKGNKYKFEPHKLYLVAGSTSAETLMFCLAEAGEAFLPTTP<br>YPGPDRDLKRRTGAELIYIHCSNPGFEKVTAALKAVOGARKHLRVKGVLVNPSN<br>PLGTMRCELDLTMTFYVKDILHSDEICSGTSDPAFGVSVMEEIGROHVSHRID<br>HVVLSLKDIKLPGRVGAIYSNNDAVAATKKMSFGIVSSOYLTVLLSPKEFT<br>KNYAENQRDKERKHEDRLVOGLRRSGISCIOSNAAGLCWDMRHLLSNTEEGEMELA<br>RKIIYOGLNISPOSSHSEPHGFRCFAAM"   |
| exon                      | <1..21<br>/gene="bac2"<br>/number=1<br>22..109<br>/gene="bac2"  |
| intron                    | /number=1<br>110..241<br>/gene="bac2"   |
| exon                      | /number=2<br>242..326<br>/gene="bac2"   |
| intron                    | /number=2<br>327..487<br>/gene="bac2"   |
| exon                      | /number=3<br>488..588<br>/gene="bac2"   |
| intron                    | /number=3<br>589..>1372<br>/gene="bac2"   |
| exon                      | /number=4   |
| BASE COUNT                | 284 a 411 c 364 g 313 t   |
| ORIGIN                    |   |
| Query Match               | 29.0%; Score 117.2; DB 8; Length 1372;  |
| Best Local Similarity     | 58.9% Pred. No. 3,4e+26;  |
| Matches 238; Conservative | 0; Mismatches 165; Indels 3; Gaps 2   |
| Oy                        | 1 GGCTGGCGGGGTTTCAGATTGGGCCGTTATCTACTCCTCAACAGAGAAGTGCTCACTACT 60<br>   <br>Db 959 GGCCCTCCGCTCCGCTCCGGGTGCATACTCACTCACACAAGAGCATGAGTGGCCGCC 1018<br><br>Oy 61 GCCAAAGATTGACGAGATTTTCATCCATTTTCAGTCGCGACGACGCGCTTGCCTCGCT 120<br>   <br>Db 1019 GCttACCAtGtgcgcttggaactcgtccctcccagacatcgaccttcctcgctt 1078<br>   <br>Oy 121 ATGCTTCGAGACAGGGGTTTCACCTAAAAAGTTTCATCGAGTAGAACAGAGCAAACTCAA 180<br>   <br>Db 1079 CTGCTCTCCGACAGAGAGTTCACAGAAACTACATTGGGAGAACCAAGAAAGGATCAAG 1138 |

| QY         | 181   | AAATATGTCCTGCATGTCGTGGCGGGGGGTGAGAAACTCGGCATTCGCATGACGGAAAG   | 240                        |
|------------|---|---|----------------------------|
| Db         | 1139  | GAGCGGACGACGCGCGCTCGT-CCAAGGCTCCGGAGAAAGCGCATCAGCTGCTGCAAG    | 1197                       |
| QY         | 241   | CAGCGAGGCTTCTGATATGTTGGCGCCGACATGACGCGGATGATTCGATTCCTACAGCGAA | 300                        |
| Db         | 1199  | CAAGCAGS--TCTGTTCTGCTGGGTGGACATGAGGACACCTGCTTAACCTCAACACGTTTC | 1255                       |
| QY         | 301   | AAAGAGAGCTTCGACCTATGGGACAAGTTGCTAAACATTGCTAAAGTAAAGTTTACTGCC  | 360                        |
| Db         | 1256  | GAGAGAGAGATGAGACTGTGGAAAGAATCGTACCAAGTGGGCTCAACATCTGCGCG      | 1315                       |
| QY         | 361   | GCTTCTTGTTGTCATGTTATGAAACCGCGCTACTTACCTCTG                    | 404                        |
| Db         | 1316  | GACTCTCTCTGCTGCACTCCACGAGCCTGGGTGTTTCGCGTCTG                  | 1359                       |
| RESULT     | 11  |   |                            |
| MSBAC1GE   |   |   |                            |
| LOCUS      | MSBAC1GE  | 1812 bp   | DNA linear PLN 18-APR-1997 |
| DEFINITION | M. acuminata bacsl gene.  |   |                            |
| ACCESSION  | X96946  |   |                            |
| VERSION    | X96946.1 GI:1945274   |   |                            |
| KEYWORDS   | 1-aminocyclopropane-1-carboxylate synthase; bacsl gene.   |   |                            |
| SOURCE     | Musa acuminata.   |   |                            |
| ORGANISM   | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; Musa.  |   |                            |
| REFERENCE  | 1 (bases 1 to 1812)   |   |                            |
| AUTHORS    | Liu, J., and Pua, E.  |   |                            |
| JOURNAL    | Unpublished   |   |                            |
| REFERENCE  | 2 (bases 1 to 1812)   |   |                            |
| AUTHORS    | Liu, J.   |   |                            |
| TITLE      | Direct Submission   |   |                            |
| JOURNAL    | Submitted (27-MAR-1996) J. Liu, Department of Botany, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, REPUBLIC OF SINGAPORE  |   |                            |
| REMARK     | revised by [3]  |   |                            |
| REFERENCE  | 3 (bases 1 to 1812)   |   |                            |
| AUTHORS    | Liu, J.   |   |                            |
| TITLE      | Direct Submission   |   |                            |
| JOURNAL    | Submitted (18-APR-1997) J. Liu, Department of Botany, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, REPUBLIC OF SINGAPORE  |   |                            |
| COMMENT    | On Apr 19, 1997 this sequence version replaced gi:1255946.  |   |                            |
| FEATURES   | Location/Qualifiers   |   |                            |
| Source     | 1..1812   |   |                            |
| gene       | /organism="Musa acuminata"  |   |                            |
| CDS        | /cultivar="AAA group, cavendish"  |   |                            |
|            | /db_xref="taxon:4641"   |   |                            |
|            | /clone_id="pbluescript KS"  |   |                            |
|            | join(308..460,551..682,767..927,1029..1812)   |   |                            |
|            | /gene="bacsl"   |   |                            |
|            | join(308..460,551..682,767..927,1029..>1812)  |   |                            |
|            | /gene="bacsl"   |   |                            |
|            | /EC_number="4.4.1.14"   |   |                            |
|            | /codon_start=1  |   |                            |
|            | /product="1-aminocyclopropane-1-carboxylate synthase"   |   |                            |
|            | /protein_id="CA65647.1"   |   |                            |
|            | /db_xref="GI:1945275"   |   |                            |
|            | /translation="MPQMLSRKACNTMGODSYFLGMEYENKPNPYDEPTNPGLIGMGLAEISDFILFESLTERHPDAGLRDCAIVRELALODYHGCLPAFKALADPAGCLGDKRKPEPKLYLTAGSTSANETLPEFLAERGEAPSPPTPYGFEDDLKWRGTAELVPHOSSNGERVTAALEKAVQGRKRLKRGVLYNPNPLGTATWTAKLELDLIFGVADIDILIDSEIYSGTFDPAFVSVMEALIEGQVSHRHVYVSLSKDLGJLGFIRGAVISNNGAVAAATKMSFGIVSSQYLLSYLSDKEFTRNHFENOKRIKRRHDRIVQGLIRSGISLCLOSNAAGLPCWMDMRMLNSDPFKGMEIMLRKIVYQVLNISPSCSCHOEDRQAFVSCFANM" |   |                            |
|            | 461..550  |   |                            |
|            | /gene="bacsl"   |   |                            |
|            | /number=1   |   |                            |
| intron     |   |   |                            |

| Query Match           | 28.2%  | Score 114:         | DB 8:           | Length 1812:    |
|-----------------------|--|--------------------|-----------------|-----------------|
| Best Local Similarity | 58.4%  | Prod. No. 3.8e-25; |                 |                 |
| Matches 236:          | Conservative   | 0:                 | Mismatches 165; | Indels 3;       |
|                       |  |                    |                 | Gaps 2;         |
| BASE COUNT            | 405 a  | 518 c              | 456 g           | 433 t           |
| ORIGIN                |  |                    |                 |                 |
| Intron                | /gene="bacs1"  |                    |                 |                 |
|                       | /number=2  |                    |                 |                 |
|                       | 928..1028  |                    |                 |                 |
|                       | /gene="bacs1"  |                    |                 |                 |
|                       | /number=3  |                    |                 |                 |
| 1                     | GGGTGCGCGGGGTTGAGATWGGGCGCTTTATCTTCTCTCTCAACGAGAGAGTGCTCACTACT   | 60                 |                 |                 |
| Db                    | 1399 GGCCTCCCTCCGCTTCCGGGTGGGTGCATCTACTCAAAACAGGGGCGAGTAGTGGCCGCC  | 1458               |                 |                 |
| Qy                    | 61 GCGAAAGATTGACGAGATTTTTCATTCATTTCACTCCGACGCGCTTGCCTCGTT  | 120                |                 |                 |
| Db                    | 1459 GCTACCAAGATGTGAGCTTTGAGCTCTCTCTCCAGACTACGTACTCTCTCGCTT  | 1518               |                 |                 |
| Qy                    | 121 ATGCTCTGGACACCGGCTTCACTCAAAAGTTTCATCGAGATACAGAGCGCAACTCAA  | 180                |                 |                 |
| Db                    | 1519 CTGCTCTCGAATAAGATGTTCACAGAAACTACATTTTCGAAACACAGAAAGATTAAG   | 1578               |                 |                 |
| Qy                    | 181 AGAATGTACGCTGCACTTGTGGCGGGGTTGAGAAACTCGCATCCGATCCAGCGGAAG  | 240                |                 |                 |
| Db                    | 1579 GAGAGCGACGACGCGGCTCGT-CCAAGGCTCCCGAGAAAGCGGCACTGCTCTGAGAG   | 1637               |                 |                 |
| Qy                    | 241 CAGCGAGGCTTCTCTATTTGTTGGGCGACATGACGCGATTGATTCCTACAGCGAA  | 300                |                 |                 |
| Db                    | 1638 CAACGCAGG--TCTGTTCTGCTGGGTGACATGAGGCACTGCTGAACCTCCGACACTTC  | 1695               |                 |                 |
| Qy                    | 301 AAAGGAGAGCTGCACCTTATGAGGAGCAAGTTCGAAACATTGCTAAGTTAAGTTACTGCC   | 360                |                 |                 |
| Db                    | 1656 AAAGGAGAGATGAGACTGTGAGAGATGATGTATCAAGTGGAGCATTAACATCTGCGCG  | 1755               |                 |                 |
| Qy                    | 361 GGTTCCTGTGTGATTTGATTTGAAACCCGCGACTTTTACCTCTGTG   | 404                |                 |                 |
| Db                    | 1756 GGCCTCTTCGTGCGCACTGCGAGAACCGGGGGTGTTCACAGCTGTG  | 1799               |                 |                 |
| RESULT 12             |  |                    |                 |                 |
| AF312737              |  |                    |                 |                 |
| LOCUS                 | AF312737   | 1400 bp            | mRNA            | linear          |
| DEFINITION            | Malus x domestica ACC synthase mRNA, partial cds.  |                    |                 | PLN 01-NOV-2000 |
| ACCESSION             | AF312737   |                    |                 |                 |
| VERSION               | AF312737.1   | GI:11066995        |                 |                 |
| KEYWORDS              |  |                    |                 |                 |
| SOURCE                |  |                    |                 |                 |
| ORGANISM              | Malus x domestica.   |                    |                 |                 |
| REFERENCE             | Malus x domestica  |                    |                 |                 |
| AUTHORS               | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eustosids I; Rosales; Rosaceae; Maloideae; Malus. |                    |                 |                 |
| TITLE                 | 1 (bases 1 to 1400)  |                    |                 |                 |
|                       | Trivedi,P.K. and Solomos,T.  |                    |                 |                 |
|                       | An apple (Malus domestica L. Borkh cv Granny Smith) ACC synthase   |                    |                 |                 |
|                       | partial cDNA   |                    |                 |                 |
|                       | unpublished  |                    |                 |                 |
|                       | 2 (bases 1 to 1400)  |                    |                 |                 |
|                       | Trivedi,P.K. and Solomos,T.  |                    |                 |                 |
|                       | Direct Submission  |                    |                 |                 |
|                       | Submitted (12-OCT-2000) NRSU, University of Maryland, Plant Science  |                    |                 |                 |
|                       | Building, College Park, MD 20742, USA  |                    |                 |                 |
|                       | location/Qualifiers  |                    |                 |                 |
|                       | 1..1400  |                    |                 |                 |
|                       | /organism="Malus x domestica"  |                    |                 |                 |
|                       | /cultivar="Granny Smith"   |                    |                 |                 |
|                       | /db_xref="taxon:3750"  |                    |                 |                 |
|                       | /tissue_type="fruit"   |                    |                 |                 |
|                       | /dev_stage="ripening"  |                    |                 |                 |
|                       | /note="authority: Malus domestica L. Borkh"  |                    |                 |                 |
|                       | <1..1385   |                    |                 |                 |

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/product="ACC synthase"
/protein_id="AAG28795.1"
/db_xref="GI:11066996"
/translation="GODSSYFLGMOEYKPNYHEVHTNGIIOMGLAENOLCPDLES
WLKNEPAARFKNGESIFAEFLFODYHGLPAFKRAMVDFMAEIRGNKYTFEPNHY
LTGATSNSETPIECIADDEAVLIPYYPGDRDLKMRTEGVEIPIHCTSSNGFOI
TETALEBAIOEAKRNIRKXGVLYTPNSPLGCTMTNRNELXLLSFVEKGIHLNDE
ITSGTAFSSPSFISVMEVLKRNCDENSEWQVHVYISLKDGLGPRVGAITSND
DMVVAATKMSFGLVSSQTHLSAMLSDRLKTKNYIAENHRLKQROKRLVSLQK
SGISCLNGNAGLCVWMDRHLRSNTFEAMELMKRYVEVHLNISPGSSCHCTEPM
FRVCPANLPERTLDLMOURLKAFVGEYVNPVEVNGSSSHLSHRSRSLTKWVSRLS
FDDRGPPIPR"

BASE COUNT      379 a      365 c      310 g      346 t
ORIGIN
Query Match      27.4%; Score 110.8; DB 8; Length 1400;
Best Local Similarity 57.9%; Pred. No. 3.9e-24;
Matches 234; Conservative 0; Mismatches 167; Indels 3; Gaps 2;

QY 1 GGGTTCGGGGGTTACAGATGGCGGTTATCTTACTTACCTCAACAAGAACGCTCACTACT 60
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
789 GGCCCTTCGGGGTTTCAGATTGGCGCCATCTACTCAACGACGACATGGTTGTGGCCGCC 848
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCCAAAAGTTGACGAGTTTTCATCCATTTCAGCTCGACGACGCGCTTGCTGCTGTT 120
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
849 GCTCAAAAATGTCAAGCTGTGCTTCTTCTTCTCAAACTCAGCACCCTTCTCCGCC 908
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 ATGCTTCGACACGCGGCTTCATCAAAAAGTTTCATGAGTAAACAGACGAAACTCAA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
909 ATGCTATCCGACAAAACACTCATAAGAACTAATAGCCGAAACACAAAAGACTCAA 968
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 AGAATGACGTCGATTTGCTGGCGGGGTTGAAGAAACTCGGCATCCATGCACGGAAG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
969 CAACGTCAGAAAAGCTGCTCGGCCCTT-CAGAAATCTGGCATTAAGCTGCTCAACGG 1027
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 CAGCGAGGCTTCTCTATTGTTGGCGCAGCATGAGCGGATGATTCGATTCCTACAGCGAA 300
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1028 CAATGCTGGCT--TCTTCTGTTGGTGATATGAGGCACTTGCTTAGGTCACACCTTT 1085
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 301 AAAGAGAGCTCGAGCTATGGAGACAGTTGCTAAACATTGCTAAGGTAAACGTTACTCC 360
    || || || || || ||||| || || || || || || || || || || || || || || || ||
1086 GAAGCCGAAATGAGCTCTGGAAAAGATTGATACGAAGTTCACCTCAATATATCTCT 1145
    || || || || || ||||| || || || || || || || || || || || || || || || ||

QY 361 GGTCTTGTTGCTGATTTGATTAACCGCGGCTACTTAAGCTCTG 404
    || || || || ||||| || || || || || || || || || || || || || || || ||
1146 GGATGCTTGTTCATTGACAGGAACTGGTTGTTCCGTCTG 1189
    || || || || ||||| || || || || || || || || || || || || || || || ||

RESULT 13
LOCUS      MSU03294      1618 bp      mRNA      linear      PLN 18-NOV-1993
DEFINITION Matus sylvestris l-aminocyclopropane-1-carboxylate synthase mRNA,
partial cds.
VERSION    U03294
KEYWORDS  U03294.1 GI:417971
SOURCE
ORGANISM  Matus sylvestris.
           Matus sylvestris
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
           Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Matus.
REFERENCE  1 (bases 1 to 1618)
           Dong,U.G., Kim,W.T., Yip,W.K., Thompson,G.A., Li,L., Bennett,A.B.
           and Yang,S.F.
           Cloning of a cDNA encoding l-aminocyclopropane-1-carboxylate
           synthase and expression of its mRNA in ripening apple fruit
           Planta 185, 38-45 (1991)
2 (bases 1 to 1618)
           Dong,U.G.
           Direct Submission
           Submitted (09-NOV-1993) Jian G. Dong, Vegetable Crops, University
           of California at Davis, Mann Lab, Davis, CA 95616-8631, USA
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FEATURES
Source
Location/Qualifiers
1..1618
/organism="Matus sylvestris"
/cultivar="Golden Delicious"
/db_xref="taxon:3732"
/clone="pAAS2"
/tissue_type="fruit"
/clone_id="Library PCGN1703"
/dev_stage="ripening"
/note="M11"
1..1618
<1..1395
/citation=[1]
CDS
old_sequence
/codon_start=1
/product="l-aminocyclopropane-1-carboxylate (ACC)
synthase"
/protein_id="AA03472.1"
/db_xref="GI:417972"
/translation="FNSHGDESSYFLGMOEYKPNYHEVHTNGIIOMGLAENOLCPD
LLESWLKNEPAARFKNGESIFAEFLFODYHGLPAFKRAMVDFMAEIRGNKYTFEPN
NHLYTPGATSNSETPIECIADDEAVLIPYYPGDRDLKMRTEGVEIPIHCTSSNGFOI
TETALEBAIOEAKRNIRKXGVLYTPNSPLGCTMTNRNELXLLSFVEKGIHLNDE
ITSGTAFSSPSFISVMEVLKRNCDENSEWQVHVYISLKDGLGPRVGAITSND
DMVVAATKMSFGLVSSQTHLSAMLSDRLKTKNYIAENHRLKQROKRLVSLQK
SGISCLNGNAGLCVWMDRHLRSNTFEAMELMKRYVEVHLNISPGSSCHCTEPM
FRVCPANLPERTLDLMOURLKAFVGEYVNPVEVNGSSSHLSHRSRSLTKWVSRLS
FDDRGPPIPR"

BASE COUNT      437 a      398 c      351 g      432 t
ORIGIN
Query Match      27.4%; Score 110.8; DB 8; Length 1618;
Best Local Similarity 57.9%; Pred. No. 4e-24;
Matches 234; Conservative 0; Mismatches 167; Indels 3; Gaps 2;

QY 1 GGGTTCGGGGGTTACAGATGGCGGTTATCTTACTTCAACAAGAACGCTCACTACT 60
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
799 GGCCCTTCGGGGTTTCAGATTGGCGCCATCTACTCAACGACGACATGGTTGTGGCCGCC 858
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCCAAAAGTTGACGAGATTTCATCCATTTCAGCTCCGACGACGCGCTTGCTGCTGTT 120
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
859 GCTCAAAAATGTCAAGCTTGTGCTTCTTCTTCTCAAACTCAGCACCCTTCTCCGCC 918
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 ATGCTTCGACACGCGGCTTCACTCAAAAAGTTTCATGAGTAAACAGACGAACTCAA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
919 ATGCTATCCGACAAAACACTCACTAAGAACTAATAGCCGAAACACAAAAGACTCAA 978
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 AGAATGACGTCGATTTGCTGGCGGGGTTGAAGAACTCGGCATCCGATGCACGGAAG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
979 CAACGTCAGAAAAGCTGCTCGGCCCTT-CAGAAATCTGGCATTAAGCTGCTCAACGG 1037
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 CAGCGAGGCTTCTCTATTGTTGGCGCAGCATGAGCGGATGATTCGATTCCTACAGCGAA 300
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1038 CAATGCTGGCT--TCTTCTGTTGGTGATATGAGGCACTTGCTTAGGTCACACCTTT 1095
    || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 301 AAAGAGAGCTCGAGCTATGGAGACAGTTGCTAAACATTGCTAAGGTAAACGTTACTCC 360
    || || || || ||||| || || || || || || || || || || || || || || || ||
1096 GAAGCCGAAATGAGCTCTGGAAAAGATTGATACGAAGTTCACCTCAATATATCTCT 1155
    || || || || ||||| || || || || || || || || || || || || || || || ||

QY 361 GGTCTTGTTGCTGATTTGATTAACCGCGGCTACTTAAGCTCTG 404
    || || || || ||||| || || || || || || || || || || || || || || || ||
1156 GGATGCTTGTTCATTGACAGGAACTGGTTGTTCCGTCTG 1199
    || || || || ||||| || || || || || || || || || || || || || || || ||

RESULT 14
LOCUS      MDO011518      1633 bp      DNA      linear      PLN 23-OCT-1998
DEFINITION Matus domestica acc synthase gene, exons 1-4, partial.
VERSION    AJ011518
KEYWORDS  AJ011518.1 GI:3790174
           1-aminocyclopropane-1-carboxylic synthase; acc synthase gene.
SOURCE
ORGANISM  Matus x domestica.
           Matus x domestica
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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## ORIGIN

Query Match 27.4%; Score 110.8; DB 8; Length 1778;  
Best Local Similarity 57.9%; Pred. No. 4e-24;  
Matches 234; Conservative 0; Mismatches 167; Indels 3; Gaps 2;

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QY 1 GGGTTGCCGGGGGTTACAGATGGCGGTTATCTACTCTACACGAGAACTGCTCCTACT 60
    || || || || || || || || || || || || || || || || || || || || ||
Db 912 GGCTTCGCCGGGTTTCGGGTTGGCGCATTTACCAACGACGACATGGTTGGCCGCC 971
QY 61 GCCAAAAAGTTGACGAGATTTTCATCCATTCCAGCTCCGACGCGCTGCTGCTGTT 120
    || || || || || || || || || || || || || || || || || || || || ||
Db 972 GCTACAAAAATGTCAGCTTTGGTCTTGTCTCTCTCAAACTCAGCACTTCTCTCCGCC 1031
QY 121 ATGCTTCGGACACGCGGTTCACTCAAAAGTTTCATCGAGGTTAAACAGAGCGAAACTCAA 180
    || || || || || || || || || || || || || || || || || || || || ||
Db 1032 ATGCTATCCGACAGAACTACTAGAACTACTAGCCGAGAACCAAAAGACTCAAA 1091
QY 181 AGAATGTACGCTGCATTGCTGGCGGGGTTGAGAAACTCGCATCCGATCGACGGAAG 240
    || || || || || || || || || || || || || || || || || || || || ||
Db 1092 CAACGTCAGAAAAATCTGCTCCGCCCTT-CAGAAAAGCTGGCATTTAGCTGCTCAATGG 1150
QY 241 CAGCGGAGGCTTCTCTATGTTGGGCCGACATGAGCGGATTCGATTCCTACAGCGAA 300
    || || || || || || || || || || || || || || || || || || || || ||
Db 1151 CAATGCTGGCT--TGTCTGTGGGTGATATGAGGCACTTGCTTAGSTCAACACCTTT 1208
QY 301 AAAGGAGAGCTGAGCTATGAGGACAAAGTTGCTAAACATTGCTAAGGTTAAACGTTACTGCC 360
    || || || || || || || || || || || || || || || || || || || || ||
Db 1209 GAAGCCGAAATGAGCTCTGSAAAAAGATGTATACGAAAGTTCAOCTCAATATCTCTCCT 1268
QY 361 GGTCTTGTGTGTCATGTATGAACCCGGCTACTTTAGCCTCTG 404
    || || || || || || || || || || || || || || || || || || || || ||
Db 1269 GGATCGTCTTGTGTCATGTCACGAACTGGTGGTTCGCTGTCG 1312
```

Search completed: March 11, 2003, 01:20:16  
Job time : 1686 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:41:37 ; Search time 1211 Seconds  
(without alignments)  
5402.953 Million cell updates/sec

Title: US-09-975-842-1

Perfect score: 404  
Sequence: 1 ggggttcgggggttcagat.....cccgctacttagcctctg 404

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estnum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_estl:\*  
10: gb\_estc2:\*  
11: gb\_hnc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_tod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 194.8 | 48.2        | 664    | 13    | BM437295 VVA017C10 |
| 2          | 174   | 43.1        | 503    | 12    | BF425479 su56c02.y |
| 3          | 168   | 41.6        | 746    | 14    | BQ118313 EST603889 |
| 4          | 164.8 | 40.8        | 480    | 10    | AW760199 s159c09.y |
| 5          | 148.4 | 36.7        | 654    | 14    | BQ764374 EBAN01.SQ |
| 6          | 147.8 | 36.6        | 685    | 10    | AV782646 AV782646  |

|   |    |       |      |      |    |                   |
|---|----|-------|------|------|----|-------------------|
| C | 7  | 145.6 | 36.0 | 550  | 14 | BM953903 sam67f01 |
|   | 8  | 143.6 | 35.5 | 629  | 13 | BJ447315          |
|   | 9  | 140   | 34.7 | 410  | 10 | BE209956          |
|   | 10 | 136.8 | 33.9 | 697  | 14 | BQ863242          |
|   | 11 | 127.6 | 31.6 | 616  | 9  | A0238159          |
|   | 12 | 119.8 | 29.7 | 515  | 10 | AM064832          |
|   | 13 | 118   | 29.2 | 483  | 10 | AM040322          |
|   | 14 | 112.6 | 27.9 | 423  | 10 | AV808550          |
|   | 15 | 107.2 | 26.5 | 420  | 10 | AV820681          |
|   | 16 | 96.8  | 23.9 | 803  | 17 | BH708432          |
|   | 17 | 96.4  | 23.0 | 1588 | 11 | AY104732          |
|   | 18 | 92.8  | 23.0 | 520  | 12 | BF648947          |
|   | 19 | 89.6  | 22.2 | 352  | 14 | BQ793884          |
|   | 20 | 87.6  | 21.7 | 700  | 14 | BQ246577          |
|   | 21 | 85.2  | 21.1 | 651  | 12 | BF649567          |
|   | 22 | 84.8  | 21.0 | 660  | 14 | BQ148323          |
|   | 23 | 83.8  | 20.7 | 656  | 9  | AL505273          |
|   | 24 | 82.2  | 20.3 | 496  | 9  | AI993687          |
|   | 25 | 82    | 20.0 | 725  | 13 | BI421967          |
|   | 26 | 80.8  | 20.0 | 725  | 14 | BQ509056          |
|   | 27 | 80.4  | 19.9 | 704  | 13 | BI921823          |
|   | 28 | 78.8  | 19.5 | 691  | 14 | BQ087604          |
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|   | 32 | 75.8  | 18.6 | 344  | 17 | CNS00PXP          |
|   | 33 | 75.2  | 18.6 | 140  | 10 | AV834755          |
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|   | 36 | 72    | 17.8 | 511  | 12 | BE821561          |
|   | 37 | 71.2  | 17.6 | 569  | 9  | AI899193          |
|   | 38 | 70.6  | 17.5 | 505  | 9  | AA650853          |
|   | 39 | 70.4  | 17.4 | 528  | 13 | BM372377          |
|   | 40 | 68.8  | 17.0 | 522  | 13 | BI315805          |
|   | 41 | 68.6  | 17.0 | 607  | 17 | B61942            |
|   | 42 | 67.6  | 16.7 | 503  | 9  | AI794804          |
|   | 43 | 64.4  | 15.9 | 658  | 9  | AI487009          |
|   | 44 | 64.2  | 15.9 | 632  | 9  | AI485399          |
|   | 45 | 64.2  | 15.9 | 636  | 9  | AI485332          |

# ALIGNMENTS

RESULT 1  
BM437295 664 bp mRNA linear EST 31-JAN-2002  
DEFINITION VVA017C10\_54085 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay  
ACCESSION CDNA Clone VVA017C10 5, mRNA sequence.  
VERSION BM437295  
KEYWORDS BM437295.1 GI:18459017  
SOURCE EST.  
ORGANISM Vitis vinifera.  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 664)  
AUTHORS Cramer,G.R. and Cushman,J.C.  
TITLE An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay  
JOURNAL Unpublished (2002)  
COMMENT Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T3 20mer  
BACKWARD: T7 21mer



```

RESULT 3
B0118313/c      746 bp      mRNA      linear      EST 17-Apr-2002
LOCUS           EST603889 mixed potato tissues Solanum tuberosum cDNA clone STMEAO1
DEFINITION      3' end, mRNA sequence.
ACCESSION      B0118313
VERSION        B0118313.1
KEYWORDS       GI:20170275
SOURCE         potato.
ORGANISM       Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 746)
AUTHORS        Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karimchyeva,S.A.
TITLE          Generation of a set of potato cDNA clones for microarray analyses
JOURNAL        Unpublished (2002)
COMMENT        Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatoflgr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdnaresgen.com
Seq primer: 17.

FEATURES
source
1..746
Location/Qualifiers
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binje"
/db_xref="taxon:4113"
/clone="STMEAO1"
/clone.lib="mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."

BASE COUNT      238 a      185 c      109 g      214 t
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Db      237      1
CAGCTTGCCATTGATGACCTGGATGTTGAG      204

RESULT 4
AM760199
LOCUS           480 bp      mRNA      linear      EST 03-DEC-2001
DEFINITION      s159c09.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl027-5609 5' similar to TR:043201 043201
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
ACCESSION      AM760199
VERSION        AM760199.1
KEYWORDS       GI:7692084
SOURCE         soybean.
ORGANISM       Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE      1 (bases 1 to 480)
AUTHORS        Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvelli,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Pearson,B., Swaller,T., Gibbons,M., Pope,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
TITLE          Public Soybean EST Project
JOURNAL        Unpublished (1999)
COMMENT        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 418.

FEATURES
source
1..480
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl027-5609"
/clone.lib="Gm-cl027"
/tissue_type="cotyledons of 3- and 7-day-old Williams
seedlings"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels with distilled
water. The cotyledons were flash-frozen in liquid
nitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthesis Kit (catalog number 200401) was used to
synthesize the cDNA. First-strand synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor
nucleotide (V=A, C, or G) was added to the 3' end of the
primer [GAGGAGAGAGAGAGAGACTACTGCGAG(T)18] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in
with cloned Pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500 bp cutoff,
using GIBCOBRL life technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript(tm) II XR Predigested vector

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[illegible]

| LOCUS                 | BE209956  | 410 bp             | mRNA      | linear      | EST 04-DEC-2001 |
|-----------------------|---|--------------------|-----------|-------------|-----------------|
| RESULT 9              |   |                    |           |             |                 |
| DEFINITION            | BE209956  | 410 bp             | mRNA      | linear      | EST 04-DEC-2001 |
| ACCESSION             | BE209956  |                    |           |             |                 |
| VERSION               | BE209956  |                    |           |             |                 |
| KEYWORDS              | EST.  |                    |           |             |                 |
| SOURCE                | soybean.  |                    |           |             |                 |
| ORGANISM              | Glycine max   |                    |           |             |                 |
| REFERENCE             | 1 (bases 1 to 410)  |                    |           |             |                 |
| AUTHORS               | Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyle, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Peterson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurr, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  |                    |           |             |                 |
| TITLE                 | Public Soybean EST Project  |                    |           |             |                 |
| JOURNAL               | Unpublished (1999)  |                    |           |             |                 |
| COMMENT               | Contact: Shoemaker R/Public Soybean EST Project<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@wustl.wustl.edu<br>This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com<br>Insert Length: 1204 Std Error: 0.00<br>High quality sequence stop: 409.  |                    |           |             |                 |
| FEATURES              |   |                    |           |             |                 |
| SOURCE                | Location/Qualifiers   |                    |           |             |                 |
|                       | 1..410  |                    |           |             |                 |
|                       | /organism="Glycine max"   |                    |           |             |                 |
|                       | /db_xref="taxon:3847"   |                    |           |             |                 |
|                       | /clone="GENOME SYSTEMS CLONE ID: Gm-cl039-110"  |                    |           |             |                 |
|                       | /clone_1lb="Gm-cl039"   |                    |           |             |                 |
|                       | /tissue_type="whole seedling without cotyledons"  |                    |           |             |                 |
|                       | /lab_host="DH10B"   |                    |           |             |                 |
|                       | /note="vector: pBluescriptII SK+, site_1: EcoRI, site_2: XhoI; This cDNA library was constructed from mRNA isolated from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Ogden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker." |                    |           |             |                 |
| BASE COUNT            | 97 a 72 c 110 g 130 t   |                    |           |             |                 |
| ORIGIN                |   |                    |           |             |                 |
| Query Match           | 34.7%   | Score 140:         | DB 10:    | Length 410: |                 |
| Best Local Similarity | 68.4%   | Pred. No. 1.le-36: |           |             |                 |
| Matches 223:          | Conservative 0:   | Mismatches 100:    | Indels 3: | Gaps 2:     |                 |
| QY                    | 79 TTTTCATCATTTTCACGCTTCGACGAGCGCTGCTGCTGTTATGCTCCGACACGCGG   | 138                |           |             |                 |
| DB                    | 1 TTCTCCACGCTTTTCGCCCAACCAAAATTGCTCATCTCCATGCTTTCAGATFCAAGT   | 60                 |           |             |                 |
| QY                    | 139 TTACACCAAAAGTTCATCAGGTTAAACAGACGAGAAACTCAAAAGATGTACGCTGCATTC  | 198                |           |             |                 |
| DB                    | 61 TTGTGTCAAAATTTATTTAGAGTTAACAGAGTTAGAGCTCGCGGAATATGTATATACATTT  | 120                |           |             |                 |
| QY                    | 199 GTGGCGGGGGTTGAACAAACTCGGCATCGCATGACGGAAGACGAGGAGCTTCTCTAT   | 258                |           |             |                 |



```

Db 121 GTGC-GGGGCTGAGACGTTGGGGATTGAGTGCACGTAGAGCACTGGTGG--TTTTCGC 177
QY 259 TGTGGGCGGACATGACGGCATTCGATTCCTACACGGAAGAGAGAGTGCAGCA 318
Db 178 TGTGGGCGTGCACATGACGAGGTGATTTGGCTCTTACAGTGAAGAGGAGAGCTTGAGCTC 237
QY 319 TGGGACAAAGTTCCTAACATTCGTAAAGTAAACGTTACTCCGGTCTTGTGTGCATTTGT 378
Db 238 TGGGATAGATTGTTGAATGTTGTAAGATCAATGTTACCCGGGGTCTCTGTGTACACTGT 297
QY 379 ATTGAACCCGGCTACTTACGCTCTG 404
Db 298 ATTGAACCTGGATGGTTTCGTTTTTG 323

RESULT 10
B0863242
LOCUS
DEFINITION B0863242 697 bp mRNA linear EST 14-AUG-2002
OCC23F17.y9.ab1 OG:ABCDI lettuce salinas Lactuca sativa CDNA clone
ACCESSION B0863242
VERSION B0863242.1 GI:22248707
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 697)
REFERENCE
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J., Ellison
,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Composite Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
CONTACT: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-752-1742
Fax: 1-(530)-752-9659
Email: akozik@catc.org [michelmore@vegmail.ucdavis.edu]
Singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: OG23 row: F column: 17.
FEATURES
source location/Qualifiers
1..697
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="OGC23F17"
/clone_lib="OG:ABCDI lettuce salinas"
/lab_host="E.coli"
/Note="Vector: pBRCDNASflAB. The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transfections made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=OG:ABCDI lettuce salinas
TAG_TISSUE=flowers post-fertilized
TAG_SEQ=TCGCATCGGC"

BASE COUNT 201 a 70 c 181 g 245 t

Query Match 33.9%; Score 136.8; DB 14; Length 697;
Best Local Similarity 62.3%; Pred. No. 1.7e-35;
Matches 248; Conservative 0; Mismatches 147; Indels 3; Gaps 2;

```

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QY 7 CCGGGGTTACAGATGGCGGTTATCTACTCTACAAAGAGACGTGCTACTAGCCAAA 66
Db 108 CCTGTTTACGAGTGGGGGTTTATTTCCTTGTGTAATAAAGCTGTGGAGCATCGAAG 167
QY 67 AAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGACGCGCTGCTGCTTAATGCTC 126
Db 168 AAATGATGAGATTTTCATCTGTCATCTTGAACCAAGATCTGCTTTCATCATCTT 227
QY 127 TCGGACAGCGGTTTACATCAAAAGTTTCATCGAGTTAAACAGACGCAAACTCAAGAATG 186
Db 228 AATGATTCAGATTTGTTGAAGGTTTATMAAGATTATAGAGAAAGATTGAGAAATG 287
QY 187 TACGCTGCATTCGTGCGCGGGGTGAGAAACTCGGCGTCATCCATCAGGAAGACGCCG 246
Db 288 AGTGATCTTTTTCGTGG-GTGTTTGAAGAGCTTTGGGAATGAGTGTATGAAGAGTGTG 346
QY 247 AGGCTTCTCTATTGTTGGGCGACATGAGCGGATTCATCCCTACAGCGAAGAGGA 306
Db 347 AGGCT--TTTATTTGTTGGCGGATTTGAGTGTTTATACGCCCTTATAGTGAAGAAAGT 404
QY 307 GAGCTCGAGCTATGGGACAAAGTTGCTAAACATTCGTTAAGTTAACGTTACTCCGTTCT 366
Db 405 GAGCTTGATTGTGGGAAAGTTGTAATGTGGGAAAGTCAATTCACCCCTGATCA 464
QY 367 TGTGTCATTTGATTGAACCCGCTACTTTCAGCCCTG 404
Db 465 TCTTGTCTATTGTGTGAACCAAGGCTTGTTAGGCTTTG 502

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```

RESULT 11
AU238159
LOCUS
DEFINITION AU238159 RAF16 Arabidopsis thaliana cDNA clone RAF16-89-D04 5',
mRNA sequence.
ACCESSION AU238159
VERSION AU238159.1 GI:19877328
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 616)
REFERENCE
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sekurai,T., Carninci,P., Kawai,U.,
Itoh,M., Ishii,Y., Arahawa,T., Shibata,K., Shinagawa,A., Muramatsu
,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rcc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified plasmid vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for further
details.
FEATURES
source location/Qualifiers
1..616
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF16-89-D04"
/clone_lib="RAF16"
/lab_host="DH10B"
/Note="Site_1: BamHI; Site_2: SalI; dark-grown"

```

```

BASE COUNT 172 a 99 c 154 g 188 t

Query Match 33.9%; Score 136.8; DB 14; Length 697;
Best Local Similarity 62.3%; Pred. No. 1.7e-35;
Matches 248; Conservative 0; Mismatches 147; Indels 3; Gaps 2;

```



```

/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; clon: Inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisonicotinic
acid, BTM, jasmonic acid, ethylene, fenthion, Eix,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."
BASE COUNT
ORIGIN
135 a      68 c      126 g      154 t

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|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 29.2%          | Score 118         | DB 10    | Length 483 |
| Best Local Similarity | 66.9%          | Pred. No. 4.1e-29 |          |            |
| Matches 198           | Conservative 0 | Mismatches 95     | Indels 3 | Gaps 2     |

QY 103 CAGCGCTGCTGCAGCTGTTCTCTCGCAACGGGGTTCCTCAAAAGTTCATCGAGCTA 162

Db 1 CAGAGCCATTATTAGTTGCATBTCTTTCCAGATBTCTGGGTTTCATCAAGATTTATTAGACACA 60

QY 163 AACAGAGCAAACTCAAAAGANTGTACGTGCATTTCTGGCGGGGTTGAAGAACTCG 222

Db 61 AACAGAGAGAAATTGGCCCAAAAGTCTTTGACTTATTTTGTGGCAGGTCTAAACAAT -TGGG 119

QY 223 CATCGATGCAAGGAAAGCAAGGAGGCTTCTATTTGTGTGGCGGCATCAGCGGATTG 282

Db 120 CATGCAATGCATGAAGAAAGCAAGTGCAGGC -CTGATTGCTGGGGTTAATAGAGGGGATTG 177

QY 283 ATTGCATCTACACAGCAAGAAAGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATGTCT 342

Db 178 ATTGGCCCTTATATGAAGAAAGGAGAGCTTGAGCTGTGGGAAAGCTCTGAATGTAGCT 237

QY 343 AAGGTAAACGTTACTCCCGGTCTCTGTGTGCATGTATTAACCCGGCTACTTTAG 398

Db 238 AAGATTAACGAGACTCCAGGCTCAGCTTGGCCATTGTATTAACCTGGATGTTCTAG 293

| RESULT 14  |                |                      |            |                   |                 |
|------------|----------------|----------------------|------------|-------------------|-----------------|
| AV808550/c |                |                      |            |                   |                 |
| LOCUS      | AV808550       | 423 bp               | mRNA       | linear            | EST 29-MAR-2002 |
| DEFINITION | AV808550 RAFL9 | Arabidopsis thaliana | CDNA clone | RAFL09-55-E15 3', |                 |
|            | mRNA sequence. |                      |            |                   |                 |

|           |                             |
|-----------|-----------------------------|
| ACCESSION | AV808550                    |
| VERSION   | AV808550.1                  |
| KEYWORDS  | GI:19842535                 |
| SOURCE    | EST.                        |
| ORGANISM  | thale cress.                |
|           | <i>Arabidopsis thaliana</i> |

REFERENCE  
Seki, M., Natsukawa, M., Ishida, T., Kamiya, A., Satou, M., Nakajima, M.,  
1 (pages 1 to 423)

**TITLE**  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
**JOURNAL**  
Unpublished (2002)  
**COMMENT**  
Contact: Motoaki Seki

Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBlueScript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

```

FEATURES      Location/Qualifiers
source        1..423
               /organism="Arabidopsis thaliana"

```

| BASE COUNT<br>ORIGIN | 121  | a | 101 | c | 72 | g | 129 | t |
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|                      | /db_xref="taxon:3702"                                      |   |     |   |    |   |     |   |
|                      | /clone="RAFL09-55-E15"                                     |   |     |   |    |   |     |   |
|                      | /clone_id="RAFL9"  |   |     |   |    |   |     |   |
|                      | /dev_stage="plants at various developmental stages from    |   |     |   |    |   |     |   |
|                      | germination to mature seeds"                               |   |     |   |    |   |     |   |
|                      | /lab_host="DH10B"  |   |     |   |    |   |     |   |
|                      | /note="Site_1: BamHI; Site_2: SalI; subjected to           |   |     |   |    |   |     |   |
|                      | dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 |   |     |   |    |   |     |   |
|                      | hr) treatments"  |   |     |   |    |   |     |   |

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 27.9%          | Score 112.6       | DB 10    | Length 423 |
| Best Local Similarity | 64.2%          | Pred. No. 2.8e-27 |          |            |
| Matches 201           | Conservative 0 | Mismatches 109    | Indels 3 | Gaps 2     |

|    |     |   |     |
|----|-----|---|-----|
| OY | 92  | CAGTCCGACGCACCGCTGGCTCCTCGTTAATGCTGTGGACACGCCGGTTCACGTAAAGT   | 151 |
| Dd | 423 | CACTCCACCCAACCATTTTGCTGTATTCCGCATCTCCATTCACAAAATGTTCAGAGAT    | 366 |
| OY | 152 | TCATCGAGTTAAACAGAGACGAACACTCAAAGAATGTACGCTGCATTCGTGGCGGGGTTG  | 211 |
| Dd | 363 | TGTGAAAAACCAACGACGACAGATTTGCAGAGTATCTCACGACCCTGTGG - AAGGGTTG | 308 |
| OY | 212 | AAGAACTCGGCATCCGATGCAACGGAANAAGCGGAGGCTTCTATTTGTGGCCACA       | 271 |
| Dd | 304 | AAAGAGTTAGGGATCGAGTGCACAAAGCAATGCAAGGT - TCTACTGTTGGGCTTATA   | 247 |
| OY | 272 | TGACGCGATTATTCATCTCTACACGCAAAAAGAGAGAGCTCGACCTATGGACAAAGTTGC  | 331 |
| Dd | 246 | TGCGAGGATTATTTCAATCTTACACGCAAAAAGGCGAGATTGACCTGTGAACAACGCTT   | 187 |
| OY | 332 | TAAACATTGCTAAAGCTTAACGTTACTCCGGTCTTGTGTCAATGTATTGAACCCGGCT    | 391 |
| Dd | 186 | TGAACATTGGCAACATCAANTCTACTACAGAGATCTTTGTGCATGTATGCAACACAGAT   | 127 |

|    |     |              |     |
|----|-----|--------------|-----|
| QY | 392 | ACTTAGCCTCTG | 404 |
|    |     |              |     |
| Db | 126 | GGTTCGTA     | 114 |

| LOCUS      | 420 bp   | mrna | linear | EST 01-APR-2002 |
|------------|--|------|--------|-----------------|
| AV820681   |  |      |        |                 |
| AV820681   | Arabidopsis thaliana cDNA clone RAP11-11-L09 3', |      |        |                 |
| DEFINITION | mrna sequence.                                   |      |        |                 |

|           |                             |
|-----------|-----------------------------|
| ACCESSION | AV820681                    |
| VERSION   | AV820681.1                  |
| KEYWORDS  | GI:198626600                |
| SOURCE    | EST.                        |
| ORGANISM  | thale cress.                |
|           | <i>Arabidopsis thaliana</i> |

REFERENCE  
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 420)

Seki, M., Nambu, A., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,

**TITLE**  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
**JOURNAL**  
Unpublished (2002)  
**COMMENT**  
Contact: Motoaki Seki

Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FIC-1 vector (Carlinchi et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web

site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

## FEATURES

**source**

Location/Qualifiers

1. .420

```
/organism="Arabidopsis thaliana"  
/db_xref="taxon:3702"
```

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/db_xref="taxon:3702"
/clone="RAFL1-11-L09"
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```
/clone_lib="RAFL1"
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```
/dev_stage="plants at
```

```
germination to mature seeds"
/lab host="PH10R"
```

```
/lab_host=DH10B...
/note="Site_1: BamHI;
```

treatments (dehydration, cold, high salt, ABA, heat and

105 120 +  
). Dark-grown plants"

|            |       |       |      |       |
|------------|-------|-------|------|-------|
| BASE COUNT | 122 a | 105 c | 64 g | 129 t |
| ORIGIN     |       |       |      |       |

ORIGIN

|             |        |              |        |             |
|-------------|--------|--------------|--------|-------------|
| Query Match | 26.58; | Score 107.2; | DB 10; | Length 420; |
|-------------|--------|--------------|--------|-------------|

Best Local Similarity 70.7%; Pred. No. 2e-25;

Matches 171; Conservative 0; Mismatches 68; Indels 3; Gaps 2;

163 AACAGAGCGAACTCAAAAGAATGTACGCTGCATTCTGTGGCGGGGTTGAAGAAACTCGG 222

Db 408 AACAGGCAGAGATTGCAGAGTATCTACACGGAGCTCGTG-AGGGCTTGAAGAGATTAGG 3500

QY 223 CATCCGATGCACGGAAGCAGCGAGGCTTCTCTATTGTTGGCCGACATGAGCGGATTG 282

Db 349 GATCGAGTGCACAGAAGCAATGGAGGT--TCTACTGTTGGGCTGATATGCCGAGGATTG 292

283 ATTCGATCCTACAGCGAAAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTTAACATTGCT 342

Db 291 ATTTCATCTTACAGCGAAAGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGC 232

343 AAGGTAACGTTACTCCCGGTTCTTGTGTCATTTGTATTGAACCCGGCTACTTTAGCCTC 402

Db 231 AAGATCAATGTCATACCAGGATCTTGTGTCTCACTGTATCGAACCAAGATGGTTCCGATC 172

|    |     |    |     |
|----|-----|----|-----|
| QY | 403 | TG | 404 |
|    |     | 11 |     |

Db 171 TG 170

Search completed: March 11, 2003, 01:40:14  
Job time : 1217 secs

Job time : 1217 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:11:12 ; Search time 43 Seconds

(without alignments)  
2881.335 Million cell updates/sec

Title: US-09-975-842-1

Perfect score: 404  
Sequence: 1 ggggttcgggggttcagat.....cccgcctacttagcctctg 404

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_NA:\*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID               | Description       |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1          | 194.8 | 48.2        | 1743   | 4 US-09-171-482-1   | Sequence 1, App11 |
| 2          | 98.4  | 24.4        | 4459   | 2 US-09-363-243-2   | Sequence 2, App11 |
| 3          | 98    | 24.3        | 1384   | 2 US-08-860-577-1   | Sequence 1, App11 |
| 4          | 86.6  | 21.4        | 961    | 4 US-08-846-826A-3  | Sequence 3, App11 |
| 5          | 84.6  | 20.9        | 968    | 4 US-08-846-826A-1  | Sequence 1, App11 |
| 6          | 83.8  | 20.7        | 994    | 2 US-08-860-577-7   | Sequence 7, App11 |
| 7          | 83.6  | 20.7        | 1878   | 1 US-08-724-194-3   | Sequence 3, App11 |
| 8          | 80.4  | 19.9        | 1096   | 3 US-09-043-627-9   | Sequence 7, App11 |
| 9          | 80.4  | 19.5        | 1113   | 3 US-09-043-627-7   | Sequence 9, App11 |
| 10         | 78.8  | 19.5        | 1112   | 2 US-08-632-598-1   | Sequence 1, App11 |
| 11         | 78.8  | 19.5        | 1712   | 4 US-09-231-240-1   | Sequence 1, App11 |
| 12         | 77    | 19.1        | 1080   | 3 US-09-043-627-1   | Sequence 1, App11 |
| 13         | 72.4  | 17.9        | 1945   | 1 US-08-724-194-1   | Sequence 1, App11 |
| 14         | 72.4  | 17.9        | 2040   | 2 US-08-695-412B-11 | Sequence 11, App1 |
| 15         | 72.4  | 17.9        | 2648   | 4 US-09-255-154D-11 | Sequence 11, App1 |
| 16         | 72.4  | 17.9        | 2678   | 1 US-08-724-194-2   | Sequence 11, App1 |
| 17         | 67.6  | 16.7        | 1703   | 4 US-08-378-313-18  | Sequence 2, App11 |
| 18         | 64.4  | 15.9        | 1104   | 3 US-09-043-627-3   | Sequence 18, App1 |
| 19         | 64.4  | 15.9        | 2230   | 4 US-08-378-313-24  | Sequence 24, App1 |
| 20         | 64.4  | 15.5        | 7244   | 4 US-08-378-313-26  | Sequence 26, App1 |
| 21         | 62.8  | 15.5        | 15397  | 2 US-08-673-768-1   | Sequence 1, App11 |
| 22         | 62.8  | 15.5        | 15397  | 2 US-08-673-768-1   | Sequence 1, App11 |
| 23         | 61.6  | 15.2        | 3513   | 2 US-08-463-418-1   | Sequence 1, App11 |
| 24         | 61.2  | 15.1        | 1800   | 1 US-07-809-457A-8  | Sequence 8, App11 |
| 25         | 61.2  | 15.1        | 1800   | 1 US-08-553-943-8   | Sequence 8, App11 |
| 26         | 61.2  | 15.1        | 1800   | 5 PCW-US91-09437-8  | Sequence 8, App11 |
| 27         | 59.6  | 14.8        | 1888   | 1 US-08-485-107-1   | Sequence 1, App11 |

|    |      |      |       |                      |                   |
|----|------|------|-------|----------------------|-------------------|
| 28 | 58.4 | 14.5 | 1098  | 3 US-09-043-627-5    | Sequence 5, App11 |
| 29 | 54.2 | 13.4 | 1497  | 2 US-08-860-577-11   | Sequence 11, App1 |
| 30 | 48.2 | 11.9 | 7587  | 4 US-08-378-313-22   | Sequence 22, App1 |
| 31 | 48.2 | 11.9 | 9060  | 4 US-08-378-313-20   | Sequence 20, App1 |
| 32 | 31.6 | 7.8  | 46819 | 4 US-09-453-702B-72  | Sequence 72, App1 |
| 33 | 30.4 | 7.5  | 46899 | 1 US-08-471-119A-1   | Sequence 1, App11 |
| 34 | 29.8 | 7.4  | 1473  | 4 US-09-134-001C-673 | Sequence 673, App |
| 35 | 29.8 | 7.4  | 5931  | 3 US-08-783-774-1    | Sequence 1, App1  |
| 36 | 29.8 | 7.4  | 5931  | 4 US-09-556-706B-1   | Sequence 1, App1  |
| 37 | 29.8 | 7.4  | 24417 | 2 US-08-846-762-1    | Sequence 1, App1  |
| 38 | 29.2 | 7.2  | 7218  | 1 US-08-232-463-14   | Sequence 14, App1 |
| 39 | 28.8 | 7.1  | 610   | 4 US-09-328-111-424  | Sequence 424, App |
| 40 | 28.6 | 7.1  | 15393 | 4 US-09-453-702B-191 | Sequence 191, App |
| 41 | 28.2 | 7.0  | 87563 | 4 US-09-453-702B-57  | Sequence 57, App1 |
| 42 | 27.6 | 6.8  | 1209  | 4 US-08-791-115B-24  | Sequence 24, App1 |
| 43 | 27.6 | 6.8  | 1962  | 4 US-08-791-115B-3   | Sequence 3, App11 |
| 44 | 27.4 | 6.8  | 289   | 4 US-09-007-005-17   | Sequence 17, App1 |
| 45 | 27.4 | 6.8  | 289   | 4 US-09-244-796-17   | Sequence 17, App1 |

#### ALIGNMENTS

```
RESULT 1
US-09-171-482-1
; Sequence 1, Application US/09171482A
; Patent No. 6184449
; GENERAL INFORMATION:
; APPLICANT: Ranu, Rajinder S.
; TITLE OR INVENTION: A 1-AMINO CYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
; FILE REFERENCE: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES
; CURRENT APPLICATION NUMBER: US/09/171,482A
; EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under WO98/14465; US5,824,87
; EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
; SOFTWARE: Word Perfect 6.1
; SEO ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Rosa kardinal
US-09-171-482-1

Query Match      48.2%   Score 194.8;   DB 4;   Length 1743;
Best Local Similarity 71.2%   Pred. No. 5; Se 59;
Matches 285;   Conservative 0;   Mismatches 112;   Indels 3;   Gaps 2;

QY      5  TCCCGGGGTTTCAGATGGGCGTTATCTACTCCCTCAACGAGACGTGCTCACTAGCGCA 64
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1232 TTCCAGGTTTCAGGTTGGTGCCATCTACTCTTTAACAGAAATGCTTGACTGCTGCTA 1291

QY      65 AAAAGTTGACGAGATTTTTCATCCATTTTCAGTCCGACGACGCGTTCGTCGTATGC 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1292 AAAAGTTGACAAAGTTCTCTCTATCTCCGCCCATCCCAACGGTTCCTATCTATGTC 1351

QY      125 TCCGAGACGCGGTTACCAAAAGTTCATGCGAGTAACGAGCAAGCAAACTCAAAAGAA 184
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1352 TTTCAGACCAAAATTTATGTCATAGTTTCATCGGATTAACAGAAAGGCTCCGTGGA 1411

QY      185 TGAAGCTGCAATTCGCGCGGGGTTGAAGAAATCCGATCCGATCAGCAAGAGCAGC 244
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1412 TGAATCTTAATTTGTGAC-AGGATTTAACAATTTGGGCAATGAGTGCACAAAGACAAT 1470

QY      245 GAGAGCTTCTATTTGTTGGCGGACATGAGCGGATTTGATTCCTACAGCAAAAG 304
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1471 GGGGG--TTTCTACTGTGGGACAGCTTGAGTGGGTAATTCGCTTACAGTGAAG 1528

QY      305 GAGAGCTGAGCTATGGGAGCAAGTGGCTAAACATTTGCTAAGGTAAGAGTACCCGGTT 364
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1529 GGAAGCTTGAGCTCTGGGATAGGTTGTTGAATGTAGGTAAGCTCAAGTACTCTGGAT 1588

QY      365 CTGTTGTCAATGTGAACCCGGGCTACTTTAGCCTCTG 404
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Db 1150 AGACGGTACGAGCAATTTGGGAAGGCTT-AAAGAGCAGGAGTGCAGTCTTTGAAGGG 1208  
QY 241 CAGCGAGGCTTCTATTTTGGGCGCATGAGCGGATTTGATTCCTACAGCGAA 300  
Db 1209 TAATGCAGGCTT-1GTTCTGTGGATGATTAATTTGGTTCTTGCTGACACGAAACGAA 1266  
QY 301 AAAGAGAGCTGAGCTATGAGGACAGTTGCTAAACATTTGCTAAGTAAAGCTTACTCCC 360  
Db 1267 CAAGCGAGCTCGAGCTTTGGGATGTATCTTGAAGAACATAAGCTCAATATATCTCT 1326  
QY 361 GGTCTGTGTCTATTTGATTTGAACCGGCTACTTTAGCCTCTG 404  
Db 1327 GGATCTTGCTGCATGTCTCGAGTATGATGTTTAGATTTG 1370

RESULT 4  
US-08-846-826A-3  
; Sequence 3, Application US/08846826A  
; Patent No. 6194639  
; GENERAL INFORMATION:  
; APPLICANT: Botella, Jose  
; APPLICANT: Sanewski, Garth  
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: One Commerce Square, 2005 Market Street, 22nd  
; STREET: Floor  
; City: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,826A  
; FILING DATE: 01-MAY-1997  
; CLASSIFICATION: 800  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: AU PN9582  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nadel Esq., Alan S.  
; REGISTRATION NUMBER: 27,363  
; REFERENCE/DOCKET NUMBER: 8795-11  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-965-1280  
; TELEFAX: 215-567-2991  
; TELEX: 831-494  
; INFORMATION FOR SEQ. ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 961 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..102  
; FEATURE:  
; NAME/KEY: mat-peptide  
; LOCATION: 103..194  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 195..961  
US-08-846-826A-3

Query Match 21.4%; Score 86.6; DB 4; Length 961;  
Best Local Similarity 55.9%; Pred. No. 8.4e-21;

Matches 205; Conservative 0; Mismatches 159; Indels 3; Gaps 2;  
QY 1 GGGTTGCCGGGGTTCAGATGGCGTTATCTACTCTCAACGAGAAGCTGCTCACTACT 60  
Db 567 GGGCTACCGAGCTTTCCGGTGGTCCGATACACTCCCAAAATGAGCGCGTGGTCTCCACG 626  
QY 61 GCCAAAAGTTGACGAGATTTTCATTCATTTAGCTCCGAGCGACCGCTGCTGCTT 120  
Db 627 GCGACCAAGATGTGAGCTTTGGGCTCATCTCTCTCAAACTCAGTACTTCTTGTCTTG 686  
QY 121 ATGCTCTCGACACGCGGTTCACTCAAAAGTTCAATCGAGTAAACGAGCAAACTCAAA 180  
Db 687 TTGCTCTCGACAAAGAGATTCACAGCGAATCAATAGGAGGAACAAACAGCGGT-TAG 745  
QY 181 AGAATGTACGCTCATTTGTGTGGCGGGTTGAGAACTCGCATCGATCCAGCGAAG 240  
Db 746 AGACGGCGCAAAAGCGGCTCACCGCAAGCGCTCGGACATCGATVMAACTGTTTGGAGAG 805  
QY 241 CAGCGAGGCTTCTATTTTGGGCGCATGAGCGGATTTGATTCATCTACAGCGAA 300  
Db 806 CAATGCAGGCTT-1GTTTGTGGTGGATGACATGAGGCACTTACTTAAGTAAAGCACT 863  
QY 301 AAAGAGAGCTGAGCTATGAGGACAGTTGCTAAACATTTGCTAAGTAAAGCTTACTCCC 360  
Db 864 GAAGGAGAGATGAGCTGTGGAAAGATAGTGCATGTATGGGACCTAAACATTTCTCCG 923  
QY 361 GGTCTT 367  
Db 924 GGTCTT 930

RESULT 5  
US-08-846-826A-1  
; Sequence 1, Application US/08846826A  
; Patent No. 6194639  
; GENERAL INFORMATION:  
; APPLICANT: Botella, Jose  
; APPLICANT: Sanewski, Garth  
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: One Commerce Square, 2005 Market Street, 22nd  
; STREET: Floor  
; City: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,826A  
; FILING DATE: 01-MAY-1997  
; CLASSIFICATION: 800  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: AU PN9582  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nadel Esq., Alan S.  
; REGISTRATION NUMBER: 27,363  
; REFERENCE/DOCKET NUMBER: 8795-11  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-965-1280  
; TELEFAX: 215-567-2991  
; TELEX: 831-494  
; INFORMATION FOR SEQ. ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 968 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double





FILING DATE: 01-OCT-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: SANTANGELO, LUKE  
REGISTRATION NUMBER: 31,997  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (970) 224-3100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-724-194-3

Query Match 20.7%; Score 83.6; DB 1; Length 1878;  
Best Local Similarity 53.7%; Pred. No. 1.4e-19;  
Matches 217; Conservative 0; Mismatches 184; Indels 3; Gaps 2;

OY 1 GGGTGGCCGGGTTTCAGATGGGGTTATCTACTCTACACAGAAAGTCTACTACT 60  
DB 953 GGGTTCCTTCGCTTCAGAGTGGGATTTCTACTCTACTACATGACGAGTTGTGATTTGT 1012  
OY 61 GCCAAAAGTTGACGAGATTTCATCTTCAGCTCCGACGCGCTTCGCTGCTT 120  
DB 1013 GCGCGAAAGTGTCAAGTTTCGGGCTTGTAATCCACACAACTCAGCACTATGSCATCA 1072  
OY 121 ATGCTCTCGACACGGGTTCACTCAAAAGTTCAATGACGTAACAGAGCAAACTCAA 180  
DB 1073 ATGCTCTCGACACGATGATTCGTGACACATTCATCTGTGGAGACGCGAAGAGCTAGCG 1132  
OY 181 AGAATGTACGCTCATTTGCGGGGGTTGAAGAAGTGGCATTCGATCGACAGGAAG 240  
DB 1133 AGAAGTACACACCTTCACACAGAGGCTTGCA-CAGTGAACATTTGATGCTTAAGAG 1191  
OY 241 CAGCGAGAGCTTCTCATTTGTTGGCCGACATGACGAGATTGATTCATCTTACAGCGAA 300  
DB 1192 CAATGGGGGTTATTCAT--ATGGATGACTTGAAGAGGCTTCTCAAGAGACACTTTC 1249  
OY 301 AAGGAGAGCTGACGATATGGGACAGTGTCTAACAATTGCTAAGGTAAACGTTACTCCC 360  
DB 1250 GAGCGGAGATGCTCTGTGAGAGTGTATATCATGAAATGAAAGTGTGCGCA 1309  
OY 361 GGTCTTGTGTCATGTATGTAACCGGCTACTTACGCTCTG 404  
DB 1310 GGGGCTCTGCTTCATTCCTCGGAGCCAGGSGTGTGATGAGTGTG 1353

RESULT 8  
US-09-043-627-7  
Sequence 7, Application US/09043627  
Patent No. 6124525  
GENERAL INFORMATION:  
APPLICANT: Botella, Jose Ramon  
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.  
STREET: 100 Thaneet Circle, Suite 306  
CITY: Princeton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08540-3662  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/043,627  
FILING DATE: 20-MAR-1998  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU96/00591  
FILING DATE: 20-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN5559  
FILING DATE: 20-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PN9603  
FILING DATE: 02-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bernstein, Scott N.  
REGISTRATION NUMBER: 38,827  
REFERENCE/DOCKET NUMBER: 3573-11US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-924-8555  
TELEFAX: 609-924-3036  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1096 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1095  
US-09-043-627-7

Query Match 19.9%; Score 80.4; DB 3; Length 1096;  
Best Local Similarity 53.2%; Pred. No. 1.4e-18;  
Matches 215; Conservative 0; Mismatches 186; Indels 3; Gaps 2;

OY 1 GGGTGGCCGGGTTTCAGATGGGGCTTACTACTCTACACAGAAAGTCTACTACT 60  
DB 688 GGGTTCCTTCGCTTCAGAGTGGGATTTGTATCTTATATATATGACGAGTTGTGATTTGT 747  
OY 61 GCCAAAAGTTGACGAGATTTCATCTTCAGCTCCGACGCGCTTCGCTGCTT 120  
DB 748 ATCCGCAATATGTCAAGCTTCGCTTGTGTAATCTCACAACATCAATTTACTGCTTCA 807  
OY 121 ATGCTCTCGACACGGGTTCACTCAAAAGTTCAATGACGTAACAGAGCAAACTCAA 180  
DB 808 ATGCTCTCGACAGATGATTTGTGAAAGTTTCTAGCGGAAAGCTCAAGAGGCTGCA 867  
OY 181 AGAATGTACGCTCATTTGCGGGGGTTGAAGAAGTGGCATTCGATCGACAGGAAG 240  
DB 868 AAAAGTACCATATTTTCAAAAGAGACTTG-AGAAAGTGGGATTAATGCTTGAAGG 926  
OY 241 CAGCGAGAGCTTCTCATTTGTTGGCCGACATGACGAGATTGATTCATCTTACAGCGAA 300  
DB 927 AATGCAAGS--TCTTTTCTTCGATGATGATTCGACACCTCTTCAACAAGAAAGTT 984  
OY 301 AAGGAGAGCTGACGATATGGGACAAAGTTGCTAACAATTGCTAAGGTAAACGTTACTCCC 360  
DB 985 GATGCCGAATGAAAGCTATGAGGCGACAGATTTGAAAGATGTAAGACTTAACGTTTCA 1044  
OY 361 GGTCTTGTGTCATGTATGTAACCGGCTACTTACGCTCTG 404  
DB 1045 GGGTCTCTTCAATTCGCAAGAGCGCTGTGTTGATGAGTGTG 1088

RESULT 9  
US-09-043-627-9  
Sequence 9, Application US/09043627  
Patent No. 6124525  
GENERAL INFORMATION:  
APPLICANT: Botella, Jose Ramon  
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.  
STREET: 100 Thaneet Circle, Suite 306  
CITY: Princeton

```
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/043,627
  FILING DATE: 20-MAR-1998
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/AU96/00591
    FILING DATE: 20-SEP-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: AU PMS559
    FILING DATE: 20-SEP-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: AU PN9603
    FILING DATE: 02-MAY-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Bernstein, Scott N.
    REGISTRATION NUMBER: 38,827
    REFERENCE/DOCKET NUMBER: 3573-11US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 609-924-8555
    TELEFAX: 609-924-3036
  INFORMATION FOR SEQ ID NO: 9:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1113 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..1113
US-09-043-627-9
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Query Match          19.9%; Score 80.4; DB 3; Length 1113;
Best Local Similarity 53.2%; Pred. No. 1.4e-18;
Matches 215; Conservative 0; Mismatches 186; Indels 3; Gaps 2;

QY 1 GGGTCCCGGGGTTAGAGATGGCGCTTATCTACTCTCAACAGAGACGTGCTCACTACT 60
    |||||
DB 694 GGGTCCCGAGGCTTTAGGGTGGCGCAATTATATCTATCAACAGATAGTGTGAGTTGC 753
QY 61 GCCAAAGATTGACGAGATTTTCATCTCATCTCCGACGCGGCTTGCTGCTGTT 120
    |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 754 GCGTCGAAATGTCAAGCTTGTGACTTGTATCATCACAACACTCAATTTATCGCTTCA 813
QY 121 ATGCTCTGGACACGCGGTTCACTCAAAAGTTTCATCGAGGTAAACAGACGAACCTCAA 180
    |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 814 ATGTATAGATGATGATGATTTGTGATGATGTTCACTACTGAGAGTCTAAAGGCTTGCA 873
QY 181 AGAATGTACGCTGCATGCTGTGGCGGGGTTGAAGAACTCGGCATCCGATCGACGGAAG 240
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 874 AAAAGGACAGAGCCTTC-ACATGGGGCTATCTCAAGTAGGCAATTTGGTTTAAAGAG 932
QY 241 CAGCGAGAGCTTCTCTATTGTTGGCCGACATGAGCGGAGTTGATTCCTACACGGA 300
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 933 CAATCGGGG-GCTATTTTCTGATGATTTTGATTCATCTCCCTCAAGAGCAAACTGAT 990
QY 301 AAAGAGAGCTGAGCTATGGACAAGTTTGCCTAAACATTGCTAAGTAAAGCTTACTCC 360
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 991 GAAGAGAGATAGAACTGTGGAAGTGAATCAACGAAGTTAAATTAAGTTTCTCG 1050
QY 361 GGTCTTGTGCTGATTTGATTCAGACCGGCTACTTTAGCCTTG 404
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1051 GGTCTTCTTTCATTTGCGCTATATCCAGAGATGTTTCGGGTTTG 1094
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```
RESULT 10
US-08-632-598-1
Sequence 1, Application US/08632598
Patent No. 5886164
GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHAN D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: CUSHMAN DARBY AND CUSHMAN
STREET: 1100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/632,598
  FILING DATE:
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: KOKULIS, PAUL N.
    REGISTRATION NUMBER: 16,773
    REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 861-3000
    TELEFAX: 822-0944
    TELEX: 6714627 CUSH
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1712 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: CDNA
    ORIGINAL SOURCE:
      ORGANISM: MUSA
      IMMEDIATE SOURCE:
      CLONE: ACS GENE
US-08-632-598-1
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Query Match          19.5%; Score 78.8; DB 2; Length 1712;
Best Local Similarity 53.0%; Pred. No. 6.5e-18;
Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;

QY 1 GGGTCCCGGGGTTAGAGATGGCGGCTTATCTACTCTCAACAGAGACGTGCTCACTACT 60
    |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 865 GCGTCCCTGCGTTCGCGGTGCGCTCATATATCTCTCAACAGAGCCGTGCTGACCTGC 924
QY 61 GCCAAAGATTGACGAGATTTTCATCTCATCTCCGACGCGAGCGGCTTGCTGCTGTT 120
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 925 GCGAGAGAGATGTCAAGCTTGTGACTGTGTCTGTCGACAGACGACCTCTGCTGCTCC 984
QY 121 ATGCTCTGGACACGCGGTTCACTCAAAAGTTTCATCGAGGTAAACAGACGAACCTCAA 180
    |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 985 ATGTTGGAGAGAGAGAGATTCACACGAGTTTCTTAAGCAGACGCGGAGGTTGTGC 1044
QY 181 AGAATGTACGCTGCATGCTGTGGCGGGGTTGAAGAACTCGGCATCCGATCGACGGAAG 240
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 1045 GGGCGGCGAGGCTTTTACGG-ACGCGCTCAAGGAGTGGGATTCATTTGTTGACGG 1103
QY 241 CAGCGAGAGCTTCTCTATTGTTGGCCGACATGAGCGGAGTTGATTCCTACACGGA 300
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 1104 CAACCGGGG-GCTGTCTGTGATGATGACCTTGAGCGCGTTCCTGAAGAAACGACGGTG 1161
QY 301 AAAGAGAGCTGAGCTATGGACAAGTTTGCCTAAACATTGCTAAGTAAAGCTTACTCC 360
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 1162 GAGGCGAGAGCTCGGCTGTGGCGGTTGATCATCAACGAGCTGAAGCTCAACATCTCGCG 1221
```



Db 691 GGTCTCCCCGGATTCGAGTCGGGATCGTGTATTCCTACAAAGACAGCGGTGATTGTC 750  
QY 61 GCCAAAAGTTGACGACATTTTCATTCATTTAGCTCCGACGACGCGTTCCTGCTT 120  
Db 751 GCACGACAAAGTGTGAGCTTCGGCTCGCTCGTCGCGACACAGTACTGCTGCCCC 810  
QY 121 ATGCTCTGGACACGCGGTTCTACATCAAAAGTTCAATCGAGTAAACAGAGCAAACTCAA 180  
Db 811 ATGCTATCCGCGAAGAAATTTTGGCAACATTTACTGACTGAAGCGCGAAGNGTGTGCG 870  
QY 181 AGAATGTACGCTGCATTCGTGTGGCGGGGTGAAGAACTCGCATCCGATCCGACGAAAG 240  
Db 871 GAGAGCCACAGATCTTCTTCCTCCGCGCTTGAGGAG-TCGACATCCCGCTGCTGACGG 929  
QY 241 CAGCGAGGCTTCTCTATTTGTTGGCCGACATGAGCGGATTTGATTCCTACAGCGAA 300  
Db 930 CAATGCCCGGG--TCTTCTGCTGTGATGACCTACGCGCACCTCCTCAAGAAACCCAGAA 987  
QY 301 AAAGGAGAGCTCGAGCTATGGGACAAAGTTGCTAAACATTTGCTAAGCTTAACGTTACTGCC 360  
Db 988 GACGCGAGAGCTGAGCTGTGGCGCTGATAGGAACAAATGTCAAGCTCAATGTGCCCC 1047  
QY 361 GATTCTTGTGTGATTTGATTTGAACCCGCGT 391  
Db 1048 GGTTCGTGTTTATTGGCGCGAGCCAGGTT 1078

RESULT 13  
US-08-724-194-1  
; Sequence 1, Application US/08724194  
; Patent No. 5824875  
; GENERAL INFORMATION:  
; APPLICANT: RANU, RAJINDER S.  
; TITLE OF INVENTION: ONE-ANTINOCYCLOPROPANE-1-CARBOXYLATE  
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARONITUM TO CONTROL ETHYLENE LEVELS  
; TITLE OF INVENTION: IN GERANIUMS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTANGELO LAW OFFICES PC  
; STREET: 315 WEST OAK STREET, STE 701  
; CITY: FORT COLLINS  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80521  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,194  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANTANGELO, LUKE  
; REGISTRATION NUMBER: 31,997  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 224-3100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1945 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-724-194-1

Query Match 17.9%; Score 72.4; DB 1; Length 1945;  
Best Local Similarity 53.7%; Pred.No.1,3e-15;  
Matches 217; Conservative 0; Mismatches 181; Indels 6; Gaps 3;  
QY 1 GGGTTGCGGGGTTGAGATGGCGCTTATCTACTCTACACAGAGAGCTGCTACTACT 60  
|| |||| ||||| | | | | ||||| | ||||| ||||| | |

Db 918 GGCATCCCCGGGTTCCGGCTCGGATCGTGTACTATTCATTAACGACGAGCTGATCCTGC 977  
QY 61 GCCAAAAGTTGACGACATTTTCATTCATTTAGCTCCGACGACGCGTTCCTGCTT 120  
Db 978 GCACGACAAAGTGTGAGCTTCGGCTCGCTCGTCGCGACACAGTACTGCTGCCCC 1037  
QY 121 ATGCTCTGGACACGCGGTTCTACATCAAAAGTTCAATCGAGTAAACAGAGCAAACTCAA 180  
Db 1038 ATGCTATCCGCGAAGAAATTTTGGCAACATTTACTGACTGAAGCGCGAAGNGTGTGCG 1094  
QY 181 AGAATGTACGCTGCATTCGTGTGGCGGGGTGAAGAACTCGCATCCGATCCGACGAAAG 240  
Db 1095 AGGAGGACAGCGGCTGTGTACGAAAGGCGTCG-AGGAGTTGGGGAATTTGATTTAAAGAG 1153  
QY 241 CAGCGAGGCTTCTCTATTTGTTGGCGCGACATGAGCGGATTTGATTCGATTCACAGCGAA 300  
Db 1154 CAACCGGG--GCTCTACTTCTGATGATTTTGGCGAAGCTTCTAGAAAGAGACGTTT 1211  
QY 301 AAAGGAGAGCTCGAGCTATGGGACAAAGTTGCTAAACATTTGCTAAGCTTAACGTTACTGCC 360  
Db 1212 GAGCGGAGAGTGTGCTGTGGAAGTGATTTATATGAGGTAAACGTTAAGCTGTCTCCG 1271  
QY 361 GATTCTTGTGTGATTTGATTTGAACCCGCGCTTACGCTGTG 404  
Db 1272 GGGTGTGCTTTCATTTGCTGTGAGCGCGGGTGTGTTAGGGTTTG 1315

RESULT 14  
US-08-695-412B-11  
; Sequence 11, Application US/08695412B  
; Patent No. 5874269  
; GENERAL INFORMATION:  
; APPLICANT: STILES, JOHN I.  
; APPLICANT: MOISYADI, STEFAN  
; TITLE OF INVENTION: NEUPANE, KABI R.  
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT  
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE  
; TITLE OF INVENTION: RIPENING OF COFFEE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JONES, DAY, REAVIS & POCUE  
; STREET: NORTH POINT, 901 LAKESIDE AVENUE  
; CITY: CLEVELAND  
; STATE: OHIO  
; COUNTRY: USA  
; ZIP: 44114  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS v. 5.1  
; SOFTWARE: WordPerfect v. 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,412B  
; FILING DATE: 12-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/485,107  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRIFFITH, CALVIN P.  
; REGISTRATION NUMBER: 34,831  
; REFERENCE/DOCKET NUMBER: 26503660002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 586-7050  
; TELEFAX: (216) 579-0212  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2040 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA to mRNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 178..1653  
US-08-695-412B-11

Query Match 17.9%; Score 72.4; DB 2; Length 2040;  
Best Local Similarity 52.0%; Pred. No. 1.3e-15;  
Matches 210; Conservative 0; Mismatches 191; Indels 3; Gaps 2;

QY 1 GGGTTCGGGGGTTTCAGAGATGGCGGTTATCTACTCTACACAGAGAACTGCTCACTACT 60  
DB 1027 GGCTTCCTCGATTTCAGAGATGGCGGTTATCTACTCTACACAGAGAACTGCTCACTACT 1086  
QY 61 GCCAAAAAGTTGACAGAGATTTTCATCTTCAGCTCCGACGCGCTTGCCTGCTT 120  
DB 1087 GCTAGAAAAATGTCAGATTTTCGCGCTTGTTCACACAACTCAGATTCGATTCATCA 1146  
QY 121 ATGCTTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAACAGAGGAAACTCAA 180  
DB 1147 ATGTTATCGGACAGAGATTTATGAGAACATATTCACAGAGCTCAGAGATTTAGCT 1206  
QY 181 AGATGACCTGATTCGTCGCGGGGTTGAAGAACTCGGATCCGATGCAAGGAAAG 240  
DB 1207 GCAGGATGCTTTTTCACAGAGAGACTTG-CTCAAGTGGCATTTGGCACCTTAAAAAG 1265  
QY 241 CAGCGAGGCTTCTCTATTTGTTGGCCGACATGAGCGGATTTGATCTCAAGCGAA 300  
DB 1266 CAGTGGGCGG--CTTTATTTCTGATGACTTAAGGAGACTCCTCAGGAGTCCACATTT 1323  
QY 301 AAGGAGAGCTCGAGCTATGAGGACAAAGTTCCTAAAGTTCCTAAGTAAAGTTACTCC 360  
DB 1324 GAGGCGAAAAATGGAACCTTGGAGGATCATATACATGAACTCAAGCTCAATGTTTCA 1383  
QY 361 GGTTCCTGTGTGATTTATTTGAACCGGCTACTTTAGCCTTG 404  
DB 1384 GGCTTATCTTTCCATTTGCTCAGAACCAAGATGGTTGAGAGTTTG 1427

RESULT 15  
US-09-255-154D-11  
Sequence 11, Application US/09255154D  
Patent No. 6448474  
GENERAL INFORMATION:  
APPLICANT: STILES, JOHN I.  
MOISYADI, ISTEFO  
NEUPANE, KABI R.  
TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT  
DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE  
RIPENING OF COFFEE  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JONES, DAY, REAVIS & POGUE  
STREET: NORTH POINT, 901 LAKE SIDE AVENUE  
CITY: CLEVELAND  
STATE: OHIO  
COUNTRY: USA  
ZIP: 44114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette, 3.5 inch, 1.44 Mb  
storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS v. 5.1  
SOFTWARE: WordPerfect v. 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/255,154D  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/695,412  
FILING DATE: 12-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GRIFFITH, CALVIN P.  
REGISTRATION NUMBER: 34,831

REFERENCE/DOCKET NUMBER: 265036600002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 586-7050  
TELEFAX: (216) 579-0212  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2040 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 178..1653  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-255-154D-11

Query Match 17.9%; Score 72.4; DB 4; Length 2040;  
Best Local Similarity 52.0%; Pred. No. 1.3e-15;  
Matches 210; Conservative 0; Mismatches 191; Indels 3; Gaps 2;

QY 1 GGGTTCGGGGGTTTCAGAGATGGCGGTTATCTACTCTACACAGAGAACTGCTCACTACT 60  
DB 1027 GGCTTCCTCGATTTCAGAGATGGCGGTTATCTACTCTACACAGAGAACTGCTCACTACT 1086  
QY 61 GCCAAAAAGTTGACAGAGATTTTCATCTTCAGCTCCGACGCGCTTGCCTGCTT 120  
DB 1087 GCTAGAAAAATGTCAGATTTTCGCGCTTGTTCACACAACTCAGATTCGATTCATCA 1146  
QY 121 ATGCTTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAACAGAGGAAACTCAA 180  
DB 1147 ATGTTATCGGACAGAGATTTATGAGAACATATTCACAGAGCTCAGAGATTTAGCT 1206  
QY 181 AGATGACCTGATTCGTCGCGGGGTTGAAGAACTCGGATCCGATGCAAGGAAAG 240  
DB 1207 GCAGGATGCTTTTTCACAGAGAGACTTG-CTCAAGTGGCATTTGGCACCTTAAAAAG 1265  
QY 241 CAGCGAGGCTTCTCTATTTGTTGGCCGACATGAGCGGATTTGATCTCAAGCGAA 300  
DB 1266 CAGTGGGCGG--CTTTATTTCTGATGACTTAAGGAGACTCCTCAGGAGTCCACATTT 1323  
QY 301 AAGGAGAGCTCGAGCTATGAGGACAAAGTTCCTAAAGTTCCTAAGTAAAGTTACTCC 360  
DB 1324 GAGGCGAAAAATGGAACCTTGGAGGATCATATACATGAACTCAAGCTCAATGTTTCA 1383  
QY 361 GGTTCCTGTGTGATTTATTTGAACCGGCTACTTTAGCCTTG 404  
DB 1384 GGCTTATCTTTCCATTTGCTCAGAACCAAGATGGTTGAGAGTTTG 1427

Search completed: March 11, 2003, 01:19:55  
Job time : 48 secs





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QY 185 TGTACGCTGATTCGTGGCGGGTTGAAGAACTCGCATCCGATGCAGGAAAGCAGC 244
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1412 TGTATCTTGATTTGTGAC-AGGATTTGAAGCAATTTGGCATTTAGTGCACAAAGACGAA 1470
QY 245 GGAAGCTTCTATTTTGTGGCCGCAGATGACGCGATTGATTCCTTACAGCGAAAG 304
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1471 GGGGG--TTTCTATCTTGGGCGAGACTTGAGTGGTTAATTCCTCTTACAGTGAAGAA 1528
QY 305 GAGAGTCGAGCTATGGGACAACTGCTAAACCTTCTAAGTAAGTAACGTTACCCGGTT 364
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1529 GGGAGCTTGAGCTGTGGATAGTTGTGAATGTAGTAAGTCAATGTTACTCTGTGAT 1588
QY 365 CTTCCTGCTATTTGATTTGAACCGGCTACTTACCTCTG 404
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1589 CTTCCTGCTATTTGATTTGAACCGGATGTTCCGCTTTTG 1628

RESULT 2
US-09-770-149-16/c
; Sequence 16, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieger, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(748)
; OTHER INFORMATION: n - A,T,C or G
US-09-770-149-16

Query Match 26.6%; Score 107.6; DB 10; Length 748;
Best Local Similarity 57.4%; Pred. No. 3,1e-27;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;
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QY 497 ATGTTGCGGATAGGAGATTACGAGAACTACATTAAGTAAACCGGAAACCTTAGA 438
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 181 AGAATGACGCTCATTCGTGCGGGGTTGAAGAACTCGCATCCGATGCAGGAAG 240
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 437 AGAGGTCAGCATACCAATTTGGGAAGGCTT-AAGAAAGCGAGGATTTAGTGTGAAG 379
QY 241 CAGCGGAGGCTTCTATTTGTTGGCGGACATAGGCGGATTTGATTCCTACAGGAA 300
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 378 GAAGCAGG--GCTATTTGTTGATGATTTGGTTTCTTGTGCGAAAGAAACTAA 321
QY 301 AAAGGAGCTCGAGCTATGGGACAAAGTTGCTAAACATTTGTAAGTAAAGTTACTCC 360
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 320 GACGGGAGCTCCAGCTTTGGATGTGATCTTAAAGAGCTGAACCTGAATATATCTCC 261
QY 361 GGTTCCTTGTGATTTGATTTGAACCGGCTACTTACCTCTG 404
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 260 GGATCTTGTGCTGCCACGTGCGAGGTGCGATGGTTAGGCTTTG 217

RESULT 3
US-09-938-842A-1571
; Sequence 1571, Application US/0993842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1571
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1571

Query Match 26.6%; Score 107.6; DB 9; Length 1344;
Best Local Similarity 57.4%; Pred. No. 4,2e-27;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;
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Db 1159 GACGGCAGCTCCAGCTTTGGATGTGATCTTAAAGAGCTGAACCTGAATATATCTCCG 1218  
QY 361 GGTCTCTGTGTGATGTATTTGAACCGCGCTACTTACCTCTG 404  
Db 1219 GGATCTTCGTGCTCACTGCTCGAGGTGCGATGTTTAGGGTTTG 1262

## RESULT 4

US-09-938-842A-1726  
; Sequence 1726, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIP1300-3  
; CURRENT APPLICATION NUMBER: US/09/938, 842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227, 866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264, 647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300, 111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1726  
; LENGTH: 1488  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1726

Query Match 13.3%; Score 53.6; DB 9; Length 1488;  
Best Local Similarity 47.5%; Pred. No. 2.5e-08;

Matches 192; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

QY 1 GGGTGGCGGGGTTGAGATGGCGTTATCTACTCTACACGAGAGCTGCTCACTACT 60  
Db 847 GGTCTGCTGTTTAAAGATGGTATAGTATAGCTTACATGACAGAGGTGTTCAATC 906  
QY 61 GCCAAAAGTTGACGAGATTTTCACTTCACCTCCGACGCGCTGCTGCTGCTT 120  
Db 907 GCAAGGAAATGTCGAGTTTCGCTGTTGTCACAAACGACGAGCTTGAATCGTAAA 966  
QY 121 ATCTCTCGACACGCGCTTCACTCAAAAGTTGATCGAGGTTAAACAGGAAACTCAA 180  
Db 967 ATGTATCCCATGAAGAGTTTGTAGACGAGTTTATCCGAGAGCAAAATTCGGTTAGCT 1026  
QY 181 AGAATGACGCTGATTCGTGCGGGGGTTGAAGAAACCTCGCATCCGATGACGGAAG 240  
Db 1027 GCAAGGACGCTGAGATTAACACCGGTTTGAATGTTAGGATTTGTTGTT---AAAG 1083  
QY 241 CACGCGAGGTTCTCTATTTTGGCCGACATAGCGGATTTGATTCATCTCAAGCGAA 300  
Db 1084 GCCAAAGCCGTTGTTCTTGTGATGATTTAAGAAATCTTTTGAAGACAGCAAGCTTT 1143  
QY 301 AAAGGAGAGCTGAGCTATGAGGACAAAGTTGCTAAACATTCGTAAAGGAAGCTTACGCC 360  
Db 1144 GATTGCGAAACGAACTATGCGCTGTGATTTGTTACACCAACTGAAGCTCAACGTTCTCCA 1203  
QY 361 GGTCTGTGTGATGTATTTGAACCCGCGCTACTTACCTCTG 404  
Db 1204 GCGGTTTCGTTCCATTTGCAATGAACCGGAGTGGTTTAGAATATG 1247

## RESULT 5

US-10-114-170-72/c  
; Sequence 72, Application US/10114170  
; Publication No. US20030023075A1  
; GENERAL INFORMATION:  
; APPLICANT: Blattner, Frederick R.

; Burland, Valerie  
; Perna, Nicole T.  
; Plunkett, Guy  
; Welch, Rod  
; TITLE OF INVENTION: No. US20030023075A1el Sequences of E. coli O157  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/114, 170  
; FILING DATE: 01-Apr-2002  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/453, 702  
; FILING DATE: 03-DEC-1999  
; APPLICATION NUMBER: 60/110, 955  
; FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27386  
; REFERENCE/DOCKET NUMBER: 960296, 95017

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 251-5000  
; TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 46819  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-10-114-170-72

Query Match 7.8%; Score 31.6; DB 9; Length 46819;  
Best Local Similarity 50.7%; Pred. No. 6.4;

Matches 76; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 198 CHTGGCGGGGTTGAAGAACTCGCATCCGATGCACGGAAGCAGCGAGCTTCTCTA 257  
Db 37493 CATCGTGGCGGTGAGGTATTTGCTGGAAGATGACAAAAAGCTTGTGACGCTGGTCTG 37434  
QY 258 TTGTGGGCCGACATGACGAGTATTGATCTCTACAGCGAAAGAGAGCTGAGCT 317  
Db 37433 AAAGCGCGCCACATGATGCGGTAAATTTTAAAAACGATCCACAAAGCATCAGAAGCA 37374  
QY 318 ATGGACAGATTTGCTAAACATTTGCTAAGGT 347  
Db 37373 GCGAAAAAGGTGCTCAGAAATGACATGCT 37344

## RESULT 6

US-09-938-842A-583  
; Sequence 583, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIP1300-3

```

; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 583
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-583
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Query Match
Best Local Similarity 57.3%; Pred. No. 2.8;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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QY 300 AAAAGAGAGCTCCAGCTATGGGACAACTTGCTAAACATTGCTAGGTAACGTTACTCC 359
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 AAAAACCTTCTCATGCTTGGCGACAGCTGATTAACAGAGTCGATTTATGCAATAG 365
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 360 CGGTTCTGTGTCATGCTATTGTAACCGGCTACTT 395
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 366 AGTTTCTTCACCGCTGATTTAAACCTGACACTT 401
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 7
US-09-920-300A-1711/c
; Sequence 1711, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1711
; LENGTH: 2302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1711
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Query Match
Best Local Similarity 51.1%; Pred. No. 4.2; DB 10; Length 2302;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
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QY 145 CAAAGTTCATCGAGGTAAACAGACGAAACTCAAAAGATGTAGCTGCATTCGTGGCG 204
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2129 CAAATTAATTAACAATPACACAGAGAGCCCTTACATGAGAAACCAATGCTTCAAGCCT 2070
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 205 GGGGTTGAAGAAGCTCGCATCCGATGCAACGAAAGCAGGAGGCTTCTATTTGTTGG 264
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2069 GGGGATGAGAGCTCTAGTCTCAAAATTTTGAACATACACATGATTTCCAGGGCAGA 2010
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 265 GCCGACATGAGCGGATTTGA 283
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2009 GAGGCTGGCTGGAGAATGA 1991
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 8
US-10-033-528-1711/c
; Sequence 1711, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
```

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; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1711
; LENGTH: 2302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1711
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Query Match
Best Local Similarity 51.1%; Pred. No. 4.2; DB 12; Length 2302;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

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QY 145 CAAAGTTCATCGAGGTAAACAGACGAAACTCAAAAGATGTAGCTGCATTCGTGGCG 204
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2129 CAAATTAATTAACAATPACACAGAGAGCCCTTACATGAGAAACCAATGCTTCAAGCCT 2070
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 205 GGGGTTGAAGAAGCTCGCATCCGATGCAACGAAAGCAGGAGGCTTCTATTTGTTGG 264
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2069 GGGGATGAGAGCTCTAGTCTCAAAATTTTGAACATACACATGATTTCCAGGGCAGA 2010
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 265 GCCGACATGAGCGGATTTGA 283
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2009 GAGGCTGGCTGGAGAATGA 1991
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 9
US-09-764-869-2327/c
; Sequence 2327, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2327
; LENGTH: 7960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2327
```

```

Query Match
Best Local Similarity 51.1%; Pred. No. 7.9; DB 10; Length 7960;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
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QY 145 CAAAGTTCATCGAGGTAAACAGACGAAACTCAAAAGATGTAGCTGCATTCGTGGCG 204
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7780 CAAATTAATTAACAATPACACAGAGAGCCCTTACATGAGAAACCAATGCTTCAAGCCT 7721
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 205 GGGGTTGAAGAAGCTCGCATCCGATGCAACGAAAGCAGGAGGCTTCTATTTGTTGG 264
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7720 GGGGATGAGAGCTCTAGTCTCAAAATTTTGAACATACACATGATTTCCAGGGCAGA 7661
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 265 GCCGACATGAGCGGATTTGA 283
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7660 GAGGCTGGCTGGAGAATGA 7642
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 10
US-09-764-869-2326/c
; Sequence 2326, Application US/09764869
; Patent No. US20020061521A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2326
; LENGTH: 17239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2326

Query Match
Best Local Similarity 7.5%; Score 30.2; DB 10; Length 17239;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 145 CAAAAGTTTCATGAGGTAACAGAGCGAAAGTCAAAAGAAATGACGCTGCTGCTGCGG 204
Db 17059 CAAAATATATACAAATATACACAGAGAGCCCTACATGAGAAAGCATGCTTCAAGCCT 17000

QY 205 GGGGTGAAGAAACCTGGCATCGATCGACGCAAGCAAGCAGCGCTTCTATTGTGG 264
Db 16999 GGGGATGAGAGCTCTAGTTCTCAATTTTAGAACATACGACATGATCTCCAGGCGAGA 16940

QY 265 GCCGACATGAGCGGATTGA 283
Db 16939 GAGGCTGCGCTGGAGAAATGA 16921

RESULT 11
US-09-924-035A-68
; Sequence 68, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Jm
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(353)
; OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-68

Query Match
Best Local Similarity 7.4%; Score 30; DB 10; Length 353;
Matches 60; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 288 ATCCATACAGCGAAAGAGAGAGCTGAGTATGGGACAAAGTTGCTTAACATTGCTAAGGT 347
Db 135 ATCAGACAAAGCAAAACAAAGAGACAGTAATGAAAGAGCTGAATCCTAAGGTTAGTG 194

QY 348 AAACGTTACTCCGGTCTGTTGTCATGTATGTGAACCCGCGCTCTTAGGC 400
Db 195 AAATTTTATACCGGTTCTTCGTATCTGAATGAAATGAAANNNTCAACTGTGCC 247

RESULT 12
US-09-954-531-90
; Sequence 90, Application US/09954531
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```
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: Gene Sets
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 291
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-291

Query Match
Best Local Similarity 7.4%; Score 29.8; DB 9; Length 398;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 145 CAAAAGTTTCATGAGGTAACAGAGCGAAAGTCAAAAGAAATGACGCTGCTGCGG 204
Db 181 CAAAATATATACAAATATACACAGAGAGCCCTACATGAGAAAGCATGCTTCAAGCCT 240

QY 205 GGGGTGAAGAAACCTGGCATCGATCGACGCAAGCAAGCAGCGGAGGCTTCTCTA 257
Db 241 GGGGATGAGAGCTCTAGTTCTCAATTTTAGAACATACGACATGATCTCCA 293

RESULT 13
US-09-954-531-291
; Sequence 291, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: Gene Sets
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 291
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-291
```

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Db      181 CAAATAATATACAAATACACAGAGAGCCCTACATGAGAAAGCCATGTGCTTCAAGCCT 240
        ||||| | | | | ||||| | | ||||| | | ||||| |
QY      205 GGGGTTGAAGAACTCGGATCCGATGCACGAAAGCGGAGGCTTCTCTA 257
        ||||| | | | | | | | | | | | | | | | | |
Db      241 GGGGATGAGGACCTCTAGTCTCAAAATCTTAGAAACATAGCACATGATTTCCCA 293
```

## RESULT 14

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US-09-954-531-508
; Sequence 508, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 508
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-508
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Query Match 7.4%; Score 29.8; DB 9; Length 398;

Best Local Similarity 54.0%; Pred. No. 2.3;

Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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QY      145 CAAAGTTTCATCGAGTAACAGAGCGAAACTCAAGAATGTACGCTGCATTCGTGGCG 204
        ||||| | | | | ||||| | | ||||| | | ||||| |
Db      181 CAAATAATATACAAATACACAGAGAGCCCTACATGAGAAAGCCATGTGCTTCAAGCCT 240
```

```
QY      205 GGGGTTGAAGAACTCGGATCCGATGCACGAAAGCGGAGGCTTCTCTA 257
        ||||| | | | | | | | | | | | | | | | | |
Db      241 GGGGATGAGGACCTCTAGTCTCAAAATCTTAGAAACATAGCACATGATTTCCCA 293
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## RESULT 15

```
US-09-962-436-152
; Sequence 152, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 152
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-152
```

Query Match 7.4%; Score 29.8; DB 10; Length 398;  
Best Local Similarity 54.0%; Pred. No. 2.3;  
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

```
QY      145 CAAAGTTTCATCGAGTAACAGAGCGAAACTCAAGAATGTACGCTGCATTCGTGGCG 204
        ||||| | | | | ||||| | | ||||| | | ||||| |
Db      181 CAAATAATATACAAATACACAGAGAGCCCTACATGAGAAAGCCATGTGCTTCAAGCCT 240
```

```
QY      205 GGGGTTGAAGAACTCGGATCCGATGCACGAAAGCGGAGGCTTCTCTA 257
        ||||| | | | | | | | | | | | | | | | | |
Db      241 GGGGATGAGGACCTCTAGTCTCAAAATCTTAGAAACATAGCACATGATTTCCCA 293
```

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Job time : 71 secs